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STIC-Biotech/ChemLib

77633

From: Li, Ruixiang  
Sent: Wednesday, October 09, 2002 4:50 PM  
To: STIC-Biotech/ChemLib  
Subject: Sequence search of Application NO:09/924,125

Please do a standard search on SEQ ID NO: 2 against both commercial and interference amino acid databases.

Thank you very much!

Ruixiang Li  
GAU 1646  
CM1 10D19  
Mail Box 10C01  
306-0282

RECEIVED  
OCT 10 2002  
STIC

Point of Contact  
P. Sheppard

Searcher: Telephone number: (703) 308-4499

Phone: \_\_\_\_\_

Location: \_\_\_\_\_

Date Picked Up: \_\_\_\_\_

Date Completed: 10/12/02

Searcher Prep/Review: \_\_\_\_\_

Clerical: \_\_\_\_\_

Online time: \_\_\_\_\_

TYPE OF SEARCH:

NA Sequences: \_\_\_\_\_

AA Sequences: \_\_\_\_\_

Structures: \_\_\_\_\_

Bibliographic: \_\_\_\_\_

Litigation: \_\_\_\_\_

Full text: \_\_\_\_\_

Patent Family: \_\_\_\_\_

Other: \_\_\_\_\_

VENDOR/COST (where applic.)

STN: \_\_\_\_\_

DIALOG: \_\_\_\_\_

Questel/Orbit: \_\_\_\_\_

DRLink: \_\_\_\_\_

Lexis/Nexis: \_\_\_\_\_

Sequence Sys.: \_\_\_\_\_

WWW/Internet: \_\_\_\_\_

Other (specify): \_\_\_\_\_

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 11, 2002, 14:45:54 Search time 33 Seconds  
(without alignments)  
1120.836 Million cell updates/sec

Title: US-09-924-125-2  
Sequence: 1 NMTTQGFNRSEKCPDRTR.....KTTASQENKSSOTDNTUG 333

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues  
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

- 1: A.Geneseq\_032802.\*
- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
- 5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*
- 6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*
- 7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*
- 8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*
- 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*
- 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*
- 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*
- 12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*
- 13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*
- 14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*
- 15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*
- 16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*
- 17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*
- 18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*
- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	1731	100.0	333 21 AAB23029	Human chemokine re
2	1731	100.0	333 22 AAB74397	Human G protein co
3	1731	100.0	333 22 AAB74494	Novel human G prot
4	1725	99.7	333 20 AAY02171	Human 7-transmembr
5	1725	99.7	333 21 AAY71299	Human orphan G pro
6	1725	99.7	333 22 AAB02833	Human G protein co
7	1725	99.7	333 22 AAU10588	Human HNEFA81 poly
8	1725	99.7	333 22 AAB31580	Amino acid sequenc
9	1710	98.8	333 22 AAE02494	Human CON203 G pro
10	1697	98.0	333 19 AAW77322	Human chemokine re
11	1402.5	81.0	336 22 AAB62472	Rat 7-transmembran

12	1372	79.3	337 22 AAB73484	Mouse G-protein-co
13	1098.5	63.5	293 17 AAB04246	Human G-protein co
14	1098.5	63.5	293 21 AAB15412	Human G-protein co
15	1098.5	63.5	293 21 AAB16735	Human G-protein co
16	829	47.9	342 20 AAB81575	EBV-induced G-prot
17	829	47.9	342 21 AAY71306	Human orphan G pro
18	829	47.9	342 21 AAB02840	Human G-protein co
19	829	47.9	342 21 AAY94444	Human 15625 recept
20	829	47.9	342 22 AAM79249	Human protein SED
21	829	47.9	342 22 AAE04386	Human p2-purinerg
22	828	47.8	342 21 AAY94445	Macaque ortholog o
23	816	46.6	343 22 AAE04385	Human p2-purinerg
24	807	46.6	343 22 AAE04384	Rat p2-purinergic
25	799	46.2	387 21 AAY94498	Rat p2-purinergic
26	777	44.9	338 21 AAY58237	Human KIAA0001 rec
27	777	44.9	338 22 AAE04388	Human UDP-glucose
28	770.5	44.3	338 21 AAY97541	Rat KIAA0001 prote
29	767.5	44.3	338 21 AAY94270	Mouse 7-transmembr
30	692.5	40.0	358 21 AAY45039	Human G-protein-co
31	692.5	40.0	358 21 AAY44365	Human G-protein-co
32	692.5	40.0	358 22 AAE03199	Human G-protein co
33	692.5	40.0	358 22 AAB96884	Human CON215 G pro
34	692.5	40.0	358 22 AAB96884	Human novel G-prot
35	692.5	40.0	358 22 AAB83014	Human G-protein co
36	692.5	40.0	358 22 AAB94659	Human protein sequ
37	692.5	40.0	358 22 AAB67484	Amino acid sequenc
38	692.5	40.0	358 22 AAB85890	Human G-protein co
39	685.5	39.6	384 22 AAB84205	Amino acid sequenc
40	677.5	39.1	358 20 AAB82820	Human G-protein co
41	674.5	39.0	358 22 AAB60692	Human G-protein-co
42	584.5	33.8	267 22 AAE04387	Human p2-purinerg
43	566	32.1	132 20 AAY12278	Human 5' EST seque
44	505.5	29.2	319 19 AAB69735	Human Csa-1-like pro
45	505.5	29.2	319 19 AAW53696	Human G-protein co

## ALIGNMENTS

RESULT 1  
ID AAB23029 standard; Protein; 333 AA.

AC AAB23029;  
DE 16-JAN-2001 (first entry)

Human chemokine receptor-like protein, SECC 2777610.

SECC protein; human; secreted; membrane-associated; cancer;  
proliferation regulator; differentiation regulator; non-malignant tumour;  
immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;  
infection; inflammatory disorder; arthritis; haematopoietic disorder;  
skin disorder; cardiovascular disorder; atherosclerosis; restenosis;  
neurological disease; Alzheimer's disease; trauma; wounding;  
spinal cord injury; skeletal disorder; cytosolic; immunosuppressive;  
anti-HIV; anti-inflamatory; anti-arteriosclerotic;  
neuroprotective; vulnery; anti-allergic; antimicrobial; cardiac;  
dermatological; gene therapy.

OS Homo sapiens.

PN WO200053742-A2.

PD 14-SEP-2000.

PF 09-MAR-2000; 2000MO-US06280.

PR 09-MAR-1999; 99US-0123667.

PR 08-MAR-2000; 2000US-0123667.

PA (CUBA-) CUBAGEN CORP.

XX

PI Shinkets RA;  
 XX  
 DR WPI: 2000-594318/56.  
 DR N-PSDB: AAA93616.  
 XX  
 PT Novel human membrane associated or secreted polypeptides and  
 PT polynucleotides useful for diagnosis, prevention and treatment of  
 PT pathological states such as cancer, immune, cardiovascular and  
 PT neurological disorders  
 XX  
 PS Claim 1; Fig 1; 151pp; English.  
 XX  
 CC Sequences AAB23029-B23048 represent human SECX proteins. The SECX  
 CC proteins of the invention are either secreted or membrane-associated  
 CC proteins and act as regulator of cellular proliferation and  
 CC differentiation. SECX proteins or nucleotides are useful for diagnosing  
 CC the presence of, or predisposition to, a disease associated with altered  
 CC levels of SECX proteins and nucleotides. The SECX proteins are also  
 CC useful to screen compounds that modulate SECX activity or expression. The  
 CC interaction of a SECX protein with other cellular proteins may be useful  
 CC to modulate the activity of a partner protein, cellular proliferation,  
 CC cellular differentiation and cell survival. SECX nucleotides are useful  
 CC for the recombinant expression of SECX protein, and may be used to detect  
 CC SECX mRNA or genetic lesions in the SECX gene. They may also be used to  
 CC modulate SECX expression (e.g., using antisense oligonucleotides). SECX  
 CC nucleic acid sequences are also useful for identifying a cell or tissue  
 CC type in a biological sample, and in forensic biology. SECX primers or  
 CC probes are useful for detecting the presence of SECX nucleotides and for  
 CC screening tissue cultures for contamination. Diseases that may be treated  
 CC or prevented using SECX proteins or nucleotides include cancer (e.g.,  
 CC colorectal carcinoma, prostate cancer), benign tumours, immune disorders  
 CC (including autoimmune diseases, transplant rejection, allergies, AIDS),  
 CC infections, inflammatory disorders, arthritis, haematopoietic disorders,  
 CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,  
 CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g.,  
 CC surgical or traumatic wounds, spinal cord injury), and skeletal  
 CC disorders.  
 CC  
 XX  
 SQ Sequence 333 AA;  
 Query Match 100.0%; Score 1731; DB 21; Length 333;  
 Best Local Similarity 100.0%; Pred. No. 6,2e-173;  
 Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNTTVMOGFNSERCPRDRIVOLVFPALYTVVFLTGILMTLAWFVHIPISSSTFIY 60  
 DB 1 MNTTVMOGFNSERCPRDRIVOLVFPALYTVVFLTGILMTLAWFVHIPISSSTFIY 60  
 QY 1 LKNTLVADLMTLMPKRIISDSHLAPWQLRAFYCRSSVTFEYTMVGYVLGLIAFDR 120  
 DB 1 LKNTLVADLMTLMPKRIISDSHLAPWQLRAFYCRSSVTFEYTMVGYVLGLIAFDR 120  
 QY 121 FLKTIIRPLRNIFLKKPVFAKTVSIFIMFEFFISLPNNILSNKEATPSSVKKCASLKGPL 180  
 DB 121 FLKTIIRPLRNIFLKKPVFAKTVSIFIMFEFFISLPNNILSNKEATPSSVKKCASLKGPL 180  
 QY 121 FLKTIIRPLRNIFLKKPVFAKTVSIFIMFEFFISLPNNILSNKEATPSSVKKCASLKGPL 180  
 DB 121 FLKTIIRPLRNIFLKKPVFAKTVSIFIMFEFFISLPNNILSNKEATPSSVKKCASLKGPL 180  
 QY 181 GLKHHQVNNICQPIETVTFILMLVFYVIAKKYDYSRKSKSDRKNNKLEGVFVVV 240  
 DB 181 GLKHHQVNNICQPIETVTFILMLVFYVIAKKYDYSRKSKSDRKNNKLEGVFVVV 240  
 QY 181 GLKHHQVNNICQPIETVTFILMLVFYVIAKKYDYSRKSKSDRKNNKLEGVFVVV 240  
 DB 181 GLKHHQVNNICQPIETVTFILMLVFYVIAKKYDYSRKSKSDRKNNKLEGVFVVV 240  
 QY 241 AVEFVCAFPFHFARVPYTHSQTNNKTCRLONOFLIAKETTLFLAATNICDPLIYIFLC 300  
 DB 241 AVEFVCAFPFHFARVPYTHSQTNNKTCRLONOFLIAKETTLFLAATNICDPLIYIFLC 300  
 QY 301 KKFTKLPKCMGKRTTASSENHSSQTDNITLG 333  
 DB 301 KKFTKLPKCMGKRTTASSENHSSQTDNITLG 333  
 RESULT 2  
 AAB74397  
 ID AAB74397 standard; Protein: 333 AA.  
 XX

AC AAB74397;  
 XX  
 XX 11-JUL-2001 (first entry)  
 DT  
 XX  
 DE Human G protein coupling receptor.  
 XX  
 XX Human; G protein coupling receptor; CNS; central nervous system.  
 KW  
 XX Homo sapiens.  
 OS  
 XX JP2001054389-A.  
 XX  
 XX 27-FEB-2001.  
 XX  
 XX 17-AUG-1999; 99JP-0230777.  
 XX  
 XX 17-AUG-1999; 99JP-0230777.  
 PR  
 XX (YAMA ) YAMANOUCHI PHARM CO LTD.  
 PA  
 XX WPI: 2001-321039/34.  
 DR  
 XX N-PSDB: AAF87601.  
 XX  
 XX A novel G protein coupling receptor.  
 PT  
 XX  
 XX  
 XX  
 XX  
 PS Claim 1; Page 11; 14pp; Japanese.  
 CC The present invention relates to a novel G protein coupling  
 CC receptor, a gene encoding for the receptor family, a process for  
 CC preparation of the receptor family, an antibody to the receptor  
 CC family and a method for screening using the receptor. The invention may  
 CC be used for screening of agents expected to be useful for  
 CC prevention and treatment of central nervous system (CNS) diseases.  
 CC The present sequence the G protein coupling receptor.  
 CC  
 XX  
 SQ Sequence 333 AA;  
 Query Match 100.0%; Score 1731; DB 22; Length 333;  
 Best Local Similarity 100.0%; Pred. No. 6,2e-173;  
 Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNTTVMOGFNSERCPRDRIVOLVFPALYTVVFLTGILMTLAWFVHIPISSSTFIY 60  
 DB 1 MNTTVMOGFNSERCPRDRIVOLVFPALYTVVFLTGILMTLAWFVHIPISSSTFIY 60  
 QY 1 LKNTLVADLMTLMPKRIISDSHLAPWQLRAFYCRSSVTFEYTMVGYVLGLIAFDR 120  
 DB 1 LKNTLVADLMTLMPKRIISDSHLAPWQLRAFYCRSSVTFEYTMVGYVLGLIAFDR 120  
 QY 121 FLKTIIRPLRNIFLKKPVFAKTVSIFIMFEFFISLPNNILSNKEATPSSVKKCASLKGPL 180  
 DB 121 FLKTIIRPLRNIFLKKPVFAKTVSIFIMFEFFISLPNNILSNKEATPSSVKKCASLKGPL 180  
 QY 121 FLKTIIRPLRNIFLKKPVFAKTVSIFIMFEFFISLPNNILSNKEATPSSVKKCASLKGPL 180  
 DB 121 FLKTIIRPLRNIFLKKPVFAKTVSIFIMFEFFISLPNNILSNKEATPSSVKKCASLKGPL 180  
 QY 181 GLKHHQVNNICQPIETVTFILMLVFYVIAKKYDYSRKSKSDRKNNKLEGVFVVV 240  
 DB 181 GLKHHQVNNICQPIETVTFILMLVFYVIAKKYDYSRKSKSDRKNNKLEGVFVVV 240  
 QY 181 GLKHHQVNNICQPIETVTFILMLVFYVIAKKYDYSRKSKSDRKNNKLEGVFVVV 240  
 DB 181 GLKHHQVNNICQPIETVTFILMLVFYVIAKKYDYSRKSKSDRKNNKLEGVFVVV 240  
 QY 241 AVEFVCAFPFHFARVPYTHSQTNNKTCRLONOFLIAKETTLFLAATNICDPLIYIFLC 300  
 DB 241 AVEFVCAFPFHFARVPYTHSQTNNKTCRLONOFLIAKETTLFLAATNICDPLIYIFLC 300  
 QY 301 KKFTKLPKCMGKRTTASSENHSSQTDNITLG 333  
 DB 301 KKFTKLPKCMGKRTTASSENHSSQTDNITLG 333  
 RESULT 3  
 AAB74494  
 ID AAB74494 standard; Protein: 333 AA.  
 XX  
 AC AAB74494;  
 XX  
 DT 31-MAY-2001 (first entry)

XX DE Novel human G protein coupled receptor.  
 XX KW Human: G protein coupled receptor; central nervous system disease;  
 XX KW schizophrenia; Parkinson's disease.  
 XX OS Homo sapiens.  
 XX PN JP2001029083-A.  
 XX PD 06-FEB-2001.  
 XX PF 23-JUL-1999; 99JP-0209918.  
 XX PR 23-JUL-1999; 99JP-0209918.  
 XX PA (YAMA ) YAMANOUCHI PHARM CO LTD.  
 XX DR WPI: 2001-221498/23.  
 XX NR N-PSDB; AAF81501.  
 XX PS A new G protein coupled receptor -  
 XX PT Example 1; Page 11; 14pp; Japanese.  
 XX CC The present invention provides the protein and coding sequences for a  
 CC novel human G protein coupled receptor. This is useful in the  
 CC identification of treatments for central nervous system diseases such as  
 CC schizophrenia, Parkinson's disease and aches.  
 XX SQ Sequence 333 AA;  
 Query Match 100.0%; Score 1731; DB 22; Length 333;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-173;  
 Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNTTVMOGFNSRERCPDRTRIVOLVFPALYVVFGLTNTLALMWVHIPSSTFIIT 60  
 DB 1 MNTTVMOGFNSRERCPDRTRIVOLVFPALYVVFGLTNTLALMWVHIPSSTFIIT 60  
 QY 61 LKNTLVADLIMTLMPKRIISDSHLAPWOLRAFCRFSVIFETMTVGIVLGLIAFDR 120  
 DB 61 LKNTLVADLIMTLMPKRIISDSHLAPWOLRAFCRFSVIFETMTVGIVLGLIAFDR 120  
 QY 121 FLKTIIRPLRNIFLKKPVFAKTVSIFIMFLEFISLPMILSNKEATPSSVKKCASLKGPL 180  
 DB 121 FLKTIIRPLRNIFLKKPVFAKTVSIFIMFLEFISLPMILSNKEATPSSVKKCASLKGPL 180  
 QY 181 GLKWHQVNNNICOFIFMTVFILMLVEFYVVIKAKYDYSRKSKSDRKNKKLEKGVFVV 240  
 DB 181 GLKWHQVNNNICOFIFMTVFILMLVEFYVVIKAKYDYSRKSKSDRKNKKLEKGVFVV 240  
 QY 241 AVFFVCAPAFPHFARVPYTHSQTNKKTDCLRLQNLFIKETTFLAATNICMDPLIYIFLC 300  
 DB 241 AVFFVCAPAFPHFARVPYTHSQTNKKTDCLRLQNLFIKETTFLAATNICMDPLIYIFLC 300  
 QY 301 KKFEKLPOMOGKRTTASSQENHSSQTDNTITG 333  
 DB 301 KKFEKLPOMOGKRTTASSQENHSSQTDNTITG 333

RESULT 4  
 AA02171  
 ID AA02171 standard; Protein; 333 AA.  
 XX AC AA02171;  
 XX DT 07-JUL-1999 (first entry)  
 XX DE Human 7-transmembrane receptor protein designated HNEA81.  
 XX KW Human 7-transmembrane receptor; HNEA81; bacterial disease; asthma;  
 KW fungal disease; viral disease; HIV-1; HIV-2; cancer; anorexia;

KW Parkinson's disease; hypertension; osteoporosis; myocardial infarction;  
 KW manic depression; schizophrenia; Gilles de la Tourette's syndrome.  
 XX OS Homo sapiens.  
 XX PN EP913471-A2.  
 XX PD 06-MAY-1999.  
 XX PF 25-AUG-1998; 98EP-0306805.  
 XX PR 23-OCT-1997; 97US-0956975.  
 XX PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX PI Halsey WS; Sathe GM;  
 XX DR WPI: 1999-256627/22.  
 XX NR N-PSDB; AAX35385.  
 XX PS Claim 11; Page 8; 20pp; English.  
 XX CC The present sequence represents a human 7-transmembrane receptor,  
 CC designated HNEA81. The products may be used in the treatment of  
 CC diseases which involve altered expression of HNEA81. These  
 CC include bacterial, fungal, or viral diseases including those  
 CC caused by HIV-1 and HIV-2, cancers, anorexia, Parkinson's disease,  
 CC hypertension, osteoporosis, myocardial infarction, asthma,  
 CC manic depression, schizophrenia and Gilles de la Tourette's syndrome.  
 XX SQ Sequence 333 AA;  
 Query Match 99.7%; Score 1725; DB 20; Length 333;  
 Best Local Similarity 99.7%; Pred. No. 2.6e-172;  
 Matches 332; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNTTVMOGFNSRERCPDRTRIVOLVFPALYVVFGLTNTLALMWVHIPSSTFIIT 60  
 DB 1 MNTTVMOGFNSRERCPDRTRIVOLVFPALYVVFGLTNTLALMWVHIPSSTFIIT 60  
 QY 61 LKNTLVADLIMTLMPKRIISDSHLAPWOLRAFCRFSVIFETMTVGIVLGLIAFDR 120  
 DB 61 LKNTLVADLIMTLMPKRIISDSHLAPWOLRAFCRFSVIFETMTVGIVLGLIAFDR 120  
 QY 121 FLKTIIRPLRNIFLKKPVFAKTVSIFIMFLEFISLPMILSNKEATPSSVKKCASLKGPL 180  
 DB 121 FLKTIIRPLRNIFLKKPVFAKTVSIFIMFLEFISLPMILSNKEATPSSVKKCASLKGPL 180  
 QY 181 GLKWHQVNNNICOFIFMTVFILMLVEFYVVIKAKYDYSRKSKSDRKNKKLEKGVFVV 240  
 DB 181 GLKWHQVNNNICOFIFMTVFILMLVEFYVVIKAKYDYSRKSKSDRKNKKLEKGVFVV 240  
 QY 241 AVFFVCAPAFPHFARVPYTHSQTNKKTDCLRLQNLFIKETTFLAATNICMDPLIYIFLC 300  
 DB 241 AVFFVCAPAFPHFARVPYTHSQTNKKTDCLRLQNLFIKETTFLAATNICMDPLIYIFLC 300  
 QY 301 KKFEKLPOMOGKRTTASSQENHSSQTDNTITG 333  
 DB 301 KKFEKLPOMOGKRTTASSQENHSSQTDNTITG 333

RESULT 5  
 AA71299  
 ID AA71299 standard; Protein; 333 AA.  
 XX AC AA71299;  
 XX DT 02-NOV-2000 (first entry)  
 XX DE Human orphan G protein-coupled receptor hARE-1.

XX Human; orphan G protein-coupled receptor; GPCR; hARE-1; drug screening;  
 KW transmembrane receptor; expressed sequence tag; EST; signal cascade.  
 XX Homo sapiens.  
 OS WO200031258-A2.  
 XX 02-JUN-2000.  
 PD 13-OCT-1999; 99WO-US23687.  
 XX 20-NOV-1998; 98US-0109213.  
 PR 16-FEB-1999; 99US-0120416.  
 PR 26-FEB-1999; 99US-0121852.  
 PR 12-MAR-1999; 99US-0123946.  
 PR 12-MAR-1999; 99US-0123949.  
 PR 28-MAY-1999; 99US-0136436.  
 PR 28-MAY-1999; 99US-0136437.  
 PR 28-MAY-1999; 99US-0136439.  
 PR 28-MAY-1999; 99US-0136567.  
 PR 28-MAY-1999; 99US-0137137.  
 PR 28-MAY-1999; 99US-0137131.  
 PR 29-JUN-1999; 99US-0114448.  
 PR 29-SEP-1999; 99US-0156555.  
 PR 29-SEP-1999; 99US-0156633.  
 PR 29-SEP-1999; 99US-0156634.  
 PR 29-SEP-1999; 99US-0156653.  
 PR 01-OCT-1999; 99US-0157280.  
 PR 01-OCT-1999; 99US-0157281.  
 PR 01-OCT-1999; 99US-0157282.  
 PR 01-OCT-1999; 99US-0157293.  
 PR 01-OCT-1999; 99US-0157294.  
 PR 12-OCT-1999; 99US-0416760.  
 PR 12-OCT-1999; 99US-0417044.  
 XX (AREN-) ARENA PHARM INC.  
 XX Chen R, Dang HT, Llaw CW, Lin I;  
 PI WPI: 2000-400068/34.  
 DR N-PSDB: AAD01126.  
 XX Novel human orphan G protein-coupled receptors and the encoding cDNAs  
 PT for use in the identification of G protein-coupled receptor agonists -  
 XX Claim 34: Page 65-66; 102pp; English.  
 XX The present amino acid sequence is the hARE-1, an endogenous human  
 CC orphan G protein-coupled receptor (GPCR), expressed in the spleen and  
 CC peripheral leucocytes. The hARE-1 cDNA was identified using EST  
 CC (expressed sequence tag) 1689643 as a probe.  
 CC The orphan GPCR of the invention, like all GPCRs, has seven transmembrane  
 CC alpha helices with an extracellular N-terminus and an intracellular  
 CC C-terminus. However, no endogenous ligands have yet been identified for  
 CC the proteins of the invention. The orphan GPCRs may be used in the  
 CC identification of their endogenous ligands, and to screen potential GPCR  
 CC agonists and antagonists for use as pharmaceutical agents. The proteins  
 CC may also be used in the study of GPCR-mediated signalling cascades, and  
 CC to elucidate their precise role in normal and diseased human conditions.  
 CC Nucleic acid encoding human orphan GPCRs may be used for tissue  
 CC localisation expression analysis to provide information about their  
 CC function in healthy and pathological states.  
 XX Sequence 333 AA;  
 SO  
 QY Query Match 99.7%; Score 1725; DB 21; Length 333;  
 Db Best Local Similarity 99.7%; Pred. No. 2, 6e-172;  
 Matches 332; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MNTVMOGFNSRCPDRTIVOLVFPALTYVFLTGILNTLALMVFVHPSSTFIIT 60  
 Db 1 MNTVMOGFNSRCPDRTIVOLVFPALTYVFLTGILNTLALMVFVHPSSTFIIT 60

QY 61 LKNTLVADLIMTLMPFLLSDSHLAPWOLRAFCRFSVIFETMYGIVLLGIADF 120  
 Db 61 LKNTLVADLIMTLMPFLLSDSHLAPWOLRAFCRFSVIFETMYGIVLLGIADF 120  
 QY 121 FLKTIIRPLRNIFELKKPVAKTVSIFIMEFFISLPNNILSKKATPSSVKKCASLKGPL 180  
 Db 121 FLKTIIRPLRNIFELKKPVAKTVSIFIMEFFISLPNNILSKKATPSSVKKCASLKGPL 180  
 QY 181 GLKHHQMVNNICQFIETVIFILMVFYVIAKVDSTIRKSKDKRNNKKLEGKVFVV 240  
 Db 181 GLKHHQMVNNICQFIETVIFILMVFYVIAKVDSTIRKSKDKRNNKKLEGKVFVV 240  
 QY 241 AVFVCFAPFHFARVPYTHSOTNNKTCRLONOLEIAKETTLELATNLCMDPLIYIFLC 300  
 Db 241 AVFVCFAPFHFARVPYTHSOTNNKTCRLONOLEIAKETTLELATNLCMDPLIYIFLC 300  
 QY 301 KKFTEKLPCKMGRKRTTASSQENHSSQTDNITLG 333  
 Db 301 KKFTEKLPCKMGRKRTTASSQENHSSQTDNITLG 333  
 RESULT 6  
 AAB02833 standard; Protein; 333 AA.  
 XX ID AAB02833  
 AC AAB02833;  
 XX 22-AUG-2000 (first entry)  
 DE Human G protein coupled receptor hARE-1 protein SEQ ID NO:20.  
 XX Human; G protein coupled receptor; GPCR; transmembrane receptor;  
 KW identification; agonist; screening; therapeutic; pharmaceutical;  
 KW mutant.  
 XX Homo sapiens.  
 OS WO200022131-A2.  
 XX 20-APR-2000.  
 PD 13-OCT-1999; 99WO-US24065.  
 XX 13-OCT-1998; 98US-0170496.  
 PR 12-NOV-1998; 98US-0108029.  
 PR 20-NOV-1998; 98US-0109213.  
 PR 27-NOV-1998; 98US-0110060.  
 PR 16-FEB-1999; 99US-0120416.  
 PR 26-FEB-1999; 99US-0121852.  
 PR 12-MAR-1999; 99US-0123944.  
 PR 12-MAR-1999; 99US-0123945.  
 PR 12-MAR-1999; 99US-0123946.  
 PR 12-MAR-1999; 99US-0123948.  
 PR 12-MAR-1999; 99US-0123949.  
 PR 12-MAR-1999; 99US-0123951.  
 PR 28-MAY-1999; 99US-0136436.  
 PR 28-MAY-1999; 99US-0136437.  
 PR 28-MAY-1999; 99US-0136439.  
 PR 28-MAY-1999; 99US-0137127.  
 PR 28-MAY-1999; 99US-0137131.  
 PR 28-MAY-1999; 99US-0137567.  
 PR 30-JUN-1999; 99US-0141448.  
 PR 27-AUG-1999; 99US-0151114.  
 PR 03-SEP-1999; 99US-0152524.  
 PR 28-SEP-1999; 99US-0156633.  
 PR 29-SEP-1999; 99US-0156555.  
 PR 29-SEP-1999; 99US-0156634.  
 XX (AREN-) ARENA PHARM INC.  
 XX Behan DP, Lehmann-Brulsma K, Chalmers DT, Chen R, Dang HT;  
 PI Gore M, Llaw CW, Lin I, Lowitz K, White C;

XX MPI: 2000-317986/27.  
 DR N-PSDB; AAA46027.  
 XX Non-endogenous, human G protein-coupled receptors for screening  
 PT receptor, inverse or partial agonists useful as therapeutic agents  
 XX Example 1; Page 94-95; 187pp; English.  
 XX The present invention describes transmembrane receptors, preferably  
 CC human G protein coupled receptors (GPCR), for which the endogenous  
 CC ligand is unknown (orphan GPCR receptors). More specifically the present  
 CC invention relates to non-endogenous, constitutively activated versions  
 CC of a human GPCR. These non-endogenous human GPCRs can be useful for  
 CC the direct identification of candidate compounds as receptors agonists,  
 CC inverse agonists or partial agonists for use as pharmaceutical agents.  
 CC AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in  
 CC the exemplification of the present invention.  
 Q Sequence 333 AA:  
 Query Match 99.7%; Score 1725; DB 21; Length 333;  
 Best Local Similarity 99.7%; Pred. No. 2,6e-172;  
 Matches 332; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Q 1 MNTVMQGFNRSERCPRDRIVOLVLPALYTVVFLGILLNTLALWVFIHPSSTFIIT 60  
 DB 1 MNTVMQGFNRSERCPRDRIVOLVLPALYTVVFLGILLNTLALWVFIHPSSTFIIT 60  
 QY 61 LKNTLVADLIMTLMPFKILSDSHLAPWOLRAFCVCRFSYVFETWYVGIYLLGLIAFDR 120  
 DB 61 LKNTLVADLIMTLMPFKILSDSHLAPWOLRAFCVCRFSYVFETWYVGIYLLGLIAFDR 120  
 QY 121 FLKIIRPLRNIFLKRVPKATYSIFTFWFLFISLPMILSNKEARPPSVKCCASLKGPL 180  
 DB 121 FLKIIRPLRNIFLKRVPKATYSIFTFWFLFISLPMILSNKEARPPSVKCCASLKGPL 180  
 QY 181 GLKHMVMNNICOFIFWTFYFILMLVYVIYAKVDSYRSKSKDKRNNKLEGGKFFVYV 240  
 DB 181 GLKHMVMNNICOFIFWTFYFILMLVYVIYAKVDSYRSKSKDKRNNKLEGGKFFVYV 240  
 QY 241 AVFVCFAPFHFARVPYTHSQTNNTKDCRLQNLFAKETTLFLAATNICMPLIYIFLC 300  
 DB 241 AVFVCFAPFHFARVPYTHSQTNNTKDCRLQNLFAKETTLFLAATNICMPLIYIFLC 300  
 QY 301 KFTTEKLPOMQGRKTTASSQENHSSOTDNITIG 333  
 DB 301 KFTTEKLPOMQGRKTTASSQENHSSOTDNITIG 333  
 RESULT 7  
 ID AAU10588 standard; Protein: 333 AA.  
 XX AAU10588;  
 XX 25-FEB-2002 (first entry)  
 DE Human HNEA81 polypeptide sequence.  
 XX Human HNEA81; G-protein coupled receptor; bacterial; infection; cancer;  
 KW fungal infection; protozoal infection; viral infection; HIV-1; HIV-2;  
 KW human immunodeficiency virus; pain; anorexia; bulimia; asthma; allergy;  
 KW Parkinson's disease; acute heart failure; hypotension; hypertension;  
 KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;  
 KW ulcer; benign prostatic hypertrophy; neurological disorder; anxiety;  
 KW schizophrenia; manic depression; dementia; delirium; psychotic disorder;  
 KW severe mental retardation; dyskinesia; Huntington's disease;  
 KW Gilles de la Tourette's syndrome.  
 XX Homo sapiens.  
 OS US2001021509-A1.  
 XX  
 PN

XX 13-SEP-2001.  
 PD 24-JAN-2001; 2001US-0769159.  
 XX 28-DEC-1998; 98US-0221456.  
 PR 26-APR-2000; 2000US-0558740.  
 PR 23-OCT-1997; 97US-0956975.  
 XX (SATH/) SATHE G M.  
 PA (HALS/) HALSEY W S.  
 PA (CHAM/) CHAMBERS J.  
 PA (MUIR/) MUIR A.  
 XX (SZERK/) SZEKERES P.  
 PI Sethe GW, Halsey WS, Chambers J, Muir A, Szekeres P.  
 XX MPI: 2001-595775/67.  
 DR N-PSDB; AAS16912.  
 XX New HNEA81 polypeptides and polynucleotides, useful for treating  
 PT infections, e.g. bacterial, fungal, protozoal and viral infections,  
 PT pain, cancers, psychotic and neurological disorders and severe mental  
 PT retardation  
 XX Claim 2; Page 6; 16pp; English.  
 XX The invention relates to the human HNEA81 polypeptide and its associated  
 CC DNA sequence. These sequences are related to the G-protein coupled  
 CC receptor family. The HNEA81 polypeptides are useful for treating  
 CC bacterial, fungal, protozoal and viral infections, particularly  
 CC infections caused by human immunodeficiency virus (HIV-1 or HIV-2, pain,  
 CC cancers, anorexia, bulimia, asthma, Parkinson's disease, acute heart  
 CC failure, hypotension, hypertension, urinary retention, osteoporosis,  
 CC angina pectoris, myocardial infarction, ulcer, allergies, benign  
 CC prostatic hypertrophy, psychotic and neurological disorders (such as  
 CC anxiety, schizophrenia, manic depression and dementia), delirium, severe  
 CC mental retardation and dyskinesias (such as Huntington's disease and  
 CC Gilles de la Tourette's syndrome). The polypeptides may also be used as  
 CC research agents and material for the discovery of treatments and  
 CC diagnostics for human and animal diseases, for screening compounds that  
 CC bind to and activate the HNEA81 polypeptides and for assessing the  
 CC binding of small molecule substrates and ligands in cells, cell-free  
 CC preparations, chemical libraries and natural product mixtures. This  
 CC sequence represents the human HNEA81 polypeptide.  
 XX SQ Sequence 333 AA:  
 Query Match 99.7%; Score 1725; DB 22; Length 333;  
 Best Local Similarity 99.7%; Pred. No. 2,6e-172;  
 Matches 332; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MNTVMQGFNRSERCPRDRIVOLVLPALYTVVFLGILLNTLALWVFIHPSSTFIIT 60  
 DB 1 MNTVMQGFNRSERCPRDRIVOLVLPALYTVVFLGILLNTLALWVFIHPSSTFIIT 60  
 QY 61 LKNTLVADLIMTLMPFKILSDSHLAPWOLRAFCVCRFSYVFETWYVGIYLLGLIAFDR 120  
 DB 61 LKNTLVADLIMTLMPFKILSDSHLAPWOLRAFCVCRFSYVFETWYVGIYLLGLIAFDR 120  
 QY 121 FLKIIRPLRNIFLKRVPKATYSIFTFWFLFISLPMILSNKEARPPSVKCCASLKGPL 180  
 DB 121 FLKIIRPLRNIFLKRVPKATYSIFTFWFLFISLPMILSNKEARPPSVKCCASLKGPL 180  
 QY 181 GLKHMVMNNICOFIFWTFYFILMLVYVIYAKVDSYRSKSKDKRNNKLEGGKFFVYV 240  
 DB 181 GLKHMVMNNICOFIFWTFYFILMLVYVIYAKVDSYRSKSKDKRNNKLEGGKFFVYV 240  
 QY 241 AVFVCFAPFHFARVPYTHSQTNNTKDCRLQNLFAKETTLFLAATNICMPLIYIFLC 300  
 DB 241 AVFVCFAPFHFARVPYTHSQTNNTKDCRLQNLFAKETTLFLAATNICMPLIYIFLC 300  
 QY 301 KFTTEKLPOMQGRKTTASSQENHSSOTDNITIG 333  
 DB 301 KFTTEKLPOMQGRKTTASSQENHSSOTDNITIG 333

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Db      301 KKFEKLPQMGGKRTTASSQENHNSQTDNTLTG 333
|||||
RESULT 8
AAB31580
ID      AAB31580 standard; Protein; 333 AA.
XX
XX      AAB31580;
XX
XX      20-APR-2001 (first entry)
XX
XX      Amino acid sequence of a human HNEA81 polypeptide.
DE
KW      Human; HNEA81; infection; pain; cancer; anorexia; bulimia; asthma;
KW      Parkinson's disease; acute heart failure; hypotension; hypertension;
KW      urinary retention; osteoporosis; angina pectoris; myocardial infarction;
KW      ulcer; asthma; allergy; benign prostatic hypertrophy; psychotic disorder;
KW      neurological disorder; anxiety; schizophrenia; manic depression;
KW      delirium; dementia; severe mental retardation; dyskinesia;
KW      Huntington's disease; Gilles de la Tourette's syndrome.
XX
XX      Homo sapiens.
XX
XX      US6162899-A.
XX
XX      19-DEC-2000.
XX
XX      28-DEC-1999; 99US-0221456.
XX
XX      23-OCT-1997; 97US-0956975.
XX
XX      (SMIK ) SMITHKLINE BEECHAM CORP.
XX      (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX      Halsey WS, Chambers J, Sathe GM, Szekeres P, Muir A;
XX
XX      WPI: 2001-090409/10.
XX      N-PSDB; AAF24909.
XX
XX      Novel human HNEA81 receptor polypeptides useful for treating microbial
XX      infections, cancer, asthma, Parkinson's disease, hypertension, urinary
XX      retention, osteoporosis, angina pectoris, myocardial infarction
XX
XX      Claim 1; Column 11-12; 16pp: English.
XX
XX      The present sequence represents a human HNEA81 polypeptide. The
XX      polypeptide is useful for the treatment of infections caused by bacterial,
XX      fungal, protozoan or viral, particularly infections caused by HIV-1 or
XX      HIV-2, pains, cancers, anorexia, bulimia, asthma, Parkinson's disease,
XX      acute heart failure, hypotension, hypertension, urinary retention,
XX      osteoporosis, angina pectoris, myocardial infarction, ulcers, asthma,
XX      allergies, benign prostatic hypertrophy, and psychotic and neurological
XX      disorders, including anxiety, schizophrenia, manic depression,
XX      delirium, dementia, severe mental retardation and dyskinesias, such as
XX      Huntington's disease or Gilles de la Tourette's syndrome.
XX
XX      Sequence 333 AA:
XX
XX      Query Match 99.7%; Score 1725; DB 22, Length 333;
XX      Best Local Similarity 99.7%; Pred. No. 2.6e-172;
XX      Matches 332; Conservative 0; Mismatches 1; Indels 0; Gaps 0
OY      1 MNTYTMQGFNSERKPRTRIVQLVFPALTYVFLTGILNTLALMVFHPHSSSTFFIT 60
OY      1 MNTYTMQGFNSERKPRTRIVQLVFPALTYVFLTGILNTLALMVFHPHSSSTFFIT 60
OY      1 LKNTLVADLIMTLMPFRIILSDSHAPQOLRAVCFRFSVYETMYGVIVLGLIAFDR 120
OY      61 LKNTLVADLIMTLMPFRIILSDSHAPQOLRAVCFRFSVYETMYGVIVLGLIAFDR 120
OY      61 LKNTLVADLIMTLMPFRIILSDSHAPQOLRAVCFRFSVYETMYGVIVLGLIAFDR 120
OY      121 FLKTRPLRNIFLKKVPVAKTVSITITWFFLEFISLPNMLISNKEATPSSVKKCAISLKGPL 180

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Dd	121	FLNIIRLRNRLNLKPPVPAKTVSIFITFLEFLISLPRTILSNKNKEALRPSSVKCASLKGVL	180
Oy	181	GLKHQWVNNICQIFEMTVETPLMLVEFYVIYAKKYDYSRKSRSKDRNNKKLEGKVYVVV	240
Dd	181	GLKHQWVNNICQIFEMTVETPLMLVEFYVIYAKKYDYSRKSRSKDRNNKKLEGKVYVVV	240
Oy	241	AVFPVCAPRFHFAVPPTHSGTNNKTKCCRIQNOLFIAKETTLPLAATNLCMPLIYIFLC	300
Dd	241	AVFPVCAPRFHFAVPPTHSGTNNKTKCCRIQNOLFIAKETTLPLAATNLCMPLIYIFLC	300
Oy	301	KKFEKLPCMOGRKTTASQENHSSQTDNTLLG	333
Dd	301	KKFEKLPCMOGRKTTASQENHSSQTDNTLLG	333
<hr/>			
RESULT 9			
XX	ID	AAE02494 standard; Protein: 333 AA.	
AC	AAE02494;		
XX	DF	10-AUG-2001 (first entry)	
XX	DE	Human CON203 G protein-coupled receptor protein.	
XX	MW	Human: G protein-coupled receptor; GPCR; CON203 protein; schizophrenia;	
KW	MW	neuroleptic; nootropic; neuroprotective; bipolar disease; psychotropic;	
KW	MW	neurological disorder; psychiatric disease; neurastis; anxiety; neuritis;	
KW	MW	attention deficit hyperactivity disorder; neurosthenia; senile dementia;	
KW	MW	affective disorder; neuropathy; Alzheimer's disease; Parkinson's disease	
XX	OS	depression; migraine; genetic screening; chromosome 3.	
XX	OS	Homo sapiens.	
XX	Key	Location/Qualifiers	
FT	FT	29..53	
FT	FT	/label= Transmembrane_domain_(1TM)	
FT	FT	54..62	
FT	FT	/label= Intracellular_domain	
FT	FT	/note= "First IC loop"	
FT	FT	63..82	
FT	FT	/label= Transmembrane_domain_(2TM)	
FT	FT	83..96	
FT	FT	/label= Extracellular_domain	
FT	FT	/note= "First EC loop"	
FT	FT	97..118	
FT	FT	/label= Transmembrane_domain_(3TM)	
FT	FT	119..135	
FT	FT	/label= Intracellular_domain	
FT	FT	/note= "Second IC loop"	
FT	FT	136..160	
FT	FT	/label= Transmembrane_domain_(4TM)	
FT	FT	161..188	
FT	FT	/label= Extracellular_domain	
FT	FT	/note= "Second EC loop"	
FT	FT	189..211	
FT	FT	/label= Transmembrane_domain_(5TM)	
FT	FT	212..231	
FT	FT	/label= Intracellular_domain	
FT	FT	/note= "Third IC loop"	
FT	FT	232..252	
FT	FT	/label= Transmembrane_domain_(6TM)	
FT	FT	253..280	
FT	FT	/label= Extracellular_domain	
FT	FT	/note= "Third EC loop"	
FT	FT	281..300	
FT	FT	/label= Transmembrane_domain_(7TM)	
XX	PD	WO200131014-A2.	
XX	PD	03-MAY-2001.	
XX	PF	27-OCT-2000; 2000WO-US29601.	



XX 27-OCT-1999; 99US-0427653.  
 PR 27-OCT-1999; 99US-0427859.  
 PR 27-OCT-1999; 99US-0428020.  
 PR 27-OCT-1999; 99US-0428114.  
 PR 28-OCT-1999; 99US-0429517.  
 PR 28-OCT-1999; 99US-0429555.  
 PR 28-OCT-1999; 99US-0429676.  
 PR 28-OCT-1999; 99US-0429695.  
 PR 03-DEC-1999; 99US-0454339.  
 PR 12-JAN-2000; 2000US-0461794.

(PHAA ) PHARMACIA & UPJOHN CO.

Vogell G, Wood LS, Merchant K;

WPI: 2001-328653/34.

DR N-PSDB; AAD06503.

Seven transmembrane receptor polypeptides and polynucleotides, useful for treating neurological or psychiatric disorders, e.g. schizophrenia, as well as for identifying compounds useful for treating schizophrenia.

Claim 1; Page 10-11; 215pp; English.

The invention relates to human G protein-coupled receptor (GPCR) and their corresponding DNA molecules. GPCR is also referred as seven transmembrane receptor. G protein-coupled receptor protein is useful for treating neurological disorder, particularly schizophrenia. GPCR protein is also useful for identifying compounds useful for treating other neurological and psychiatric diseases, e.g. depression, anxiety, bipolar disease, affective disorders, attention deficit hyperactivity disorder/attention deficit disorder, epilepsy, neuritis, neuroasthenia, neuropathy, neurosis, Alzheimer's disease, Parkinson's disease, migraine and senile dementia. The invention also provides genetic screening procedures that entail analyzing a person's genome with respect to GPCR. The vectors are useful for the recombinant production of the GPCR's. The present sequence is human CON203 G protein-coupled receptor (GPCR) protein.

Sequence 333 AA;

Query Match. Best Local Similarity 98.8%; Score 1710; DB 22; Length 333;

Matches 330; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNTVMGSEFNSRERCPDRTRIVQLVFPALTYVFLTGILNTLALMTVHPSSSTFIIT 60  
 DB 1 MNTVMGSEFNSRERCPDRTRIVQLVFPALTYVFLTGILNTLALMTVHPSSSTFIIT 60  
 QY 61 LKNTLVADLIMTLMPEKILSDSHLAPWOLRAFCRSSVIFETMYGIVLLGLIAFDR 120  
 DB 61 LKNTLVADLIMTLMPEKILSDSHLAPWOLRAFCRSSVIFETMYGIVLLGLIAFDR 120  
 QY 121 FLKTIIRPLRNIFFLKKPVFAKTVSIFIMFEFFISLPMILSNKRAITSSVKKCSLGPL 180  
 DB 121 FLKTIIRPLRNIFFLKKPVFAKTVSIFIMFEFFISLPMILSNKRAITSSVKKCSLGPL 180  
 QY 181 GLKWHQVNNICOFIFMTVETILMLVFFVYVIAKKYDSYRSKSKDRNNKKLEBKVVVV 240  
 DB 181 GLKWHQVNNICOFIFMTVETILMLVFFVYVIAKKYDSYRSKSKDRNNKKLEBKVVVV 240  
 QY 241 AVFVFCAPFHPFARVYTHSOTNNKTDCLONOLFIAKETTLFLAATNIMCDPLIYIFLC 300  
 DB 241 AVFVFCAPFHPFARVYTHSOTNNKTDCLONOLFIAKETTLFLAATNIMCDPLIYIFLC 300  
 QY 301 KKFEKLPKMOGRKTTASSOENHSSOTDNTITG 333  
 DB 301 KKFEKLPKMOGRKTTASSOENHSSOTDNTITG 333

RESULT 10

AAW77322  
 ID AAW77322 standard; Protein; 333 AA.

AC AAW77322;

DT 27-NOV-1998 (first entry)

XX Human chemokine receptor-like protein.

KW Human; chemokine receptor-like protein; NHCN; inflammatory disorder; viral infection.

OS Homo sapiens.

PN WO9839441-A1.

PD 11-SEP-1998.

PF 05-MAR-1998; 98WO-US042278.

PR 06-MAR-1997; 97US-0812871.

PA (INCY-) INCYTE PHARM INC.

PI Au-Young J, Cheng M, Guegler KJ;

DR WPI: 1998-506362/43.

DR N-PSDB; AAV59144.

PT New human chemokine receptor-like protein - is useful in the treatment of inflammatory disorders and/or viral infections

XX Claim 1; Fig 1; 60pp; English.

CC The present sequence represents a pure human chemokine receptor-like protein (NHCN). The protein can be used in methods to treat an inflammatory disorder or a viral infection.

Sequence 333 AA;

Query Match. Best Local Similarity 98.0%; Score 1697; DB 19; Length 333;

Matches 328; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MNTVMGSEFNSRERCPDRTRIVQLVFPALTYVFLTGILNTLALMTVHPSSSTFIIT 60  
 DB 1 MNTVMGSEFNSRERCPDRTRIVQLVFPALTYVFLTGILNTLALMTVHPSSSTFIIT 60  
 QY 61 LKNTLVADLIMTLMPEKILSDSHLAPWOLRAFCRSSVIFETMYGIVLLGLIAFDR 120  
 DB 61 LKNTLVADLIMTLMPEKILSDSHLAPWOLRAFCRSSVIFETMYGIVLLGLIAFDR 120  
 QY 121 FLKTIIRPLRNIFFLKKPVFAKTVSIFIMFEFFISLPMILSNKRAITSSVKKCSLGPL 180  
 DB 121 FLKTIIRPLRNIFFLKKPVFAKTVSIFIMFEFFISLPMILSNKRAITSSVKKCSLGPL 180  
 QY 181 GLKWHQVNNICOFIFMTVETILMLVFFVYVIAKKYDSYRSKSKDRNNKKLEBKVVVV 240  
 DB 181 GLKWHQVNNICOFIFMTVETILMLVFFVYVIAKKYDSYRSKSKDRNNKKLEBKVVVV 240  
 QY 241 AVFVFCAPFHPFARVYTHSOTNNKTDCLONOLFIAKETTLFLAATNIMCDPLIYIFLC 300  
 DB 241 AVFVFCAPFHPFARVYTHSOTNNKTDCLONOLFIAKETTLFLAATNIMCDPLIYIFLC 300  
 QY 301 KKFEKLPKMOGRKTTASSOENHSSOTDNTITG 333  
 DB 301 KKFEKLPKMOGRKTTASSOENHSSOTDNTITG 333

RESULT 11

AA62472  
 ID AAB62472 standard; Protein; 336 AA.

XX

AC AAB62472;  
 XX 09-JUL-2001 (first entry)  
 DT XX  
 DE Rat 7-transmembrane receptor, rhNEEA81.  
 XX  
 XX 7-transmembrane receptor; rhNEEA81; G-protein coupled receptor; GPCR;  
 KW antihIV; cytostatic; antidiabetic; anorectic; antiallergic; osteopathic;  
 KW antiparkinsonian; hypotensive; antianxiety; cerebroprotective; antitumor;  
 KW antimigraine; antiallergic; neuroprotective; antidepressant; rat;  
 KW antimicrobial; gene therapy.  
 XX  
 OS Rattus sp.  
 XX  
 PN MO200129089-A1.  
 XX  
 PD 26-APR-2001.  
 XX  
 PF 19-OCT-2000; 2000WO-US28906.  
 XX  
 PR 19-OCT-1999; 99US-0160438.  
 PR 18-OCT-2000; 2000US-0691271.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 PI  
 PI TrinH HN;  
 XX  
 DR WPI: 2001-308478/32.  
 DR N-PSDB: AAF57695.  
 XX  
 PT New rat 7-transmembrane receptor (G-protein coupled receptor (GPCR)),  
 PT rat 7-transmembrane receptor (G-protein coupled receptor (GPCR)),  
 PT cancer, diabetes, obesity, anorexia, bulimia, asthma and Parkinson's  
 PT disease  
 PS  
 PS Claim 2; Page 35; 39pp; English.  
 XX  
 CC This represents a rat 7-transmembrane receptor, rat rhNEEA81  
 CC polypeptide belonging to the family of G-protein coupled receptor (GPCR).  
 CC The rhNEEA81 is useful for treating bacterial, fungal, protozoan and  
 CC viral infections, particularly infections caused by HIV-1 or HIV-2, pain,  
 CC cancer, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's  
 CC disease, acute heart failure, hypotension, hypertension, urinary  
 CC retention, osteoporosis, angina pectoris, myocardial infarction, stroke,  
 CC ulcers, asthma, allergies, benign prostatic hypertrophy, migraine,  
 CC vomiting, psychotic and neurological disorders including anxiety,  
 CC schizophrenia, manic depression, depression, delirium, dementia and  
 CC severe mental retardation, and dyskinesias, such as Huntington's disease  
 CC or Gilles de la Tourette's syndrome.  
 AX  
 SQ Sequence 336 AA;  
 Query Match 81.08; Score 1402.5; DB 22; Length 336;  
 Best Local Similarity 80.28; Pred. No. 1.6e-138;  
 Matches 267; Conservative 29; Mismatches 34; Indels 3; Gaps 3;  
 QY 1 MNTVMGQFNSEKCPDRIQVLPALYVFLTGILNTLALWVFVHPSSTFTY 60  
 DB 5 VNTGMOGFKSEKCPDRIQVLPALYVFLTGILNTLALWVFVHPSSTFTY 64  
 QY 61 LKNTLVADLNTLMLPKRISDSHAPQQLRAEVCRESSVFETVMVGVILGLIAFDR 120  
 DB 65 LKNTLVADLNTLMLPKRISDSHAPQQLRAEVCRESSVFETVMVGVILGLIAFDR 124  
 QY 121 FLKIRIRLNFELKPPYFAKVSFFIFPFISLPMWISLNKATPSSVAKCASLGPL 180  
 DB 125 FLKIRIRLNFELKPPYFAKVSFFIFPFISLPMWISLNKATPSSVAKCASLGPL 183  
 QY 181 GLKHHQVNNICQIFMTVFILMLVFFVYLAKKYDSYRSKSKSDRNNKRLKGVVYV 240  
 DB 184 GLKHHQVNNICQIFMTVFILMLVFFVYLAKKYDSYRSKSKSDRNNKRLKGVVYV 242

QY 241 AVEVCFAPFHFARVPYTHSQTNNKTDCLONQFIKATETTLFATNICKDPLIYIFLC 300  
 DB 243 AVEVCFAPFHFARVPYTHSQTNNKTDCLONQFIKATETTLFATNICKDPLIYIFLC 302  
 QY 301 KKFTKLEPCMOGR-KTTSQGENHSSQTDNITL 332  
 DB 303 KKFTKLEPCMOGR-KTTSQGENHSSQTDNITL 335  
 RESULT 12  
 AAB73484  
 ID AAB73484 standard; Protein: 337 AA.  
 AC AAB73484;  
 XX  
 XX 09-JUL-2001 (first entry)  
 DE Mouse G protein-coupled receptor mHNEEA81.  
 XX  
 XX Mouse; mHNEEA81; G protein-coupled receptor; GPCR; 7TM receptor;  
 KW 7 transmembrane domain receptor; infection; viral; bacterial; fungal;  
 KW protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia;  
 KW bulimia; osteoporosis; asthma; allergy; urinary retention;  
 KW acute heart failure; hypotension; hypertension; angina pectoris;  
 KW myocardial infarction; stroke; ulcer; migraine; vomiting;  
 KW psychotic disorder; neurological disorder; anxiety; schizophrenia;  
 KW manic depression; bipolar disorder; depression; delirium; dementia;  
 KW severe mental retardation; dyskinesia; Parkinson's disease;  
 KW Huntington's disease; Gilles de la Tourette's syndrome;  
 KW transgenic animal; drug screening; signal transduction;  
 KW agonist; antagonist; human KINA001 homologue.  
 XX  
 OS Mus musculus.  
 XX  
 PN MO200127153-A1.  
 XX  
 PD 19-APR-2001.  
 XX  
 PF 13-OCT-2000; 2000WO-US28304.  
 PF 13-OCT-1999; 99US-0159217.  
 PR 12-OCT-2000; 2000US-0689582.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 PI  
 PI Taylor AH, Ames RS, Sarau HM, Foley JJ;  
 XX  
 DR WPI: 2001-290711/30.  
 DR N-PSDB: AAF84498.  
 XX  
 PT Mus musculus mHNEEA81 polypeptide for production of agonists and  
 PT antagonists for treatment of diseases e.g. infections, cancers,  
 PT psychotic and neurologic disorders.  
 PS  
 PS Claim 2; Page 37; 45pp; English.  
 XX  
 CC This sequence represents the mouse mHNEEA81 protein. The mouse mHNEEA81  
 CC protein is a member of the G protein-coupled receptor (GPCR) superfamily,  
 CC and like all GPCRs, mouse mHNEEA81 has 7 putative transmembrane domains  
 CC and is involved in signal transduction. In particular, mouse mHNEEA81  
 CC has homology to human KINA001. The invention also relates to expression  
 CC vectors and host cells comprising mHNEEA81 DNA, to recombinant  
 CC expression of mHNEEA81, to drug screening methods that use mouse  
 CC mHNEEA81 and to mHNEEA81 agonists and antagonists. Mouse mHNEEA81  
 CC nucleic acid sequences may be used to isolate cDNA and/or genomic clones  
 CC encoding mHNEEA81 homologues or orthologues, particularly from other  
 CC species, and may also be used in chromosome localization studies. Mouse  
 CC mHNEEA81 nucleotides may be used to generate transgenic animals,  
 CC including knockout animals, which may provide an insight into treating a  
 CC variety of human disorders. Such disorders include bacterial, fungal,  
 CC protozoal and viral infections, particularly HIV-1 or HIV-2 infections;  
 CC pain; cancers; benign prostatic hypertrophy; diabetes; obesity; anorexia;

CC bullma; osteoporosis; asthma; allergies; urinary retention; acute heart  
 CC failure; hypotension; hypertension; angina pectoris; myocardial  
 CC infarction; stroke; ulcers; migraine; vomiting; psychotic and  
 CC neurological disorders such as anxiety, schizophrenia, manic depression,  
 CC depression, delirium, dementia, and severe mental retardation, and  
 CC dyskinesias, such as Parkinson's disease, Huntington's disease or Gilles  
 CC de la Tourette's syndrome. mNENAA81 proteins and nucleotides may also be  
 CC used in screening compounds for their ability to modulate mNENAA81  
 CC activity or expression.

XX Sequence 337 AA;

Query Match 79.3%; Score 1372; DB 22; Length 337;  
 Best Local Similarity 77.8%; Pred. No. 2.6e-135;  
 Matches 260; Conservative 34; Mismatches 36; Indels 4; Gaps 3;

QY 1 MNTVMGPFNSERCPDRTRIQVLPALYVVELTGILNTLALMVFHIPSSTFIY 60  
 DB 5 INTGMOGFNSERCPDRTRIQVLPALYVVELTGILNTLALMVFHIPSSTFIY 64

Y 61 LKNTLVADLIMTLMPKILSDSHLAPMOLRAFCRFSVFEETMYGIVLLGIADR 120  
 DB 65 LKNTLVADLIMTLMPKILSDSHLAPMOLRAFCRFSVFEETMYGIVLLGIADR 124

QY 121 FLKIRPLRNIFLKKPVFAKTVSIFIMFEFISLPNNILSNKEATPSVKKASLKGPL 180  
 DB 125 FLKIRPLRNIFLKKPVFAKTVSIFIMFEFISLPNNILSNKEATPSVKKASLKGPL 183

QY 181 GLKWHQVNNICOPFEWVFTILMLVFYVIAKKYDYSRKSKDRKNNKLEGVFVV 240  
 DB 184 GLMWHQVNSHTCOPIFWAVFLMLLFYAVITKKYNSYRKRFSKDSR-HKRLGVKVFIVM 242

QY 241 AVEFVCAPRHFARVPTTHSOTNNKTCRLONOFLIAKETTLFLAANICDPLIYFLC 300  
 DB 243 AVEFVCAPRHFARVPTTHSOTNNKTCRLONOFLIAKETTLFLAANICDPLIYFLC 302

QY 301 KKEFEKLPCKMGRK--TTASOENHSSQTDNITL 332  
 DB 303 KKEFEKLPCKMGRK--TTASOENHSSQTDNITL 336

RESULT 13  
 AAM04246  
 ID AAM04246 standard; Protein; 293 AA.

XX AAM04246;  
 XX 13-DEC-1996 (first entry)

DE Human G-protein coupled receptor GPR3.  
 XX G-protein coupled receptor; GPR3; signal transduction; agonist;  
 KW antagonist; cell proliferation; cancer; tumour; asthma; allergy;  
 XX diagnosis.

XX Homo sapiens.  
 OS  
 XX WO9630406-A1.

XX 03-OCT-1996.  
 PD 30-MAR-1995; 95MO-US04079.  
 XX 30-MAR-1995; 95MO-US04079.

XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX Built CJ, Cao L, Gentz R, Li Y, Ni J, Rosen CA;  
 PI Sutton GG;

XX MPI; 1996-455278/45.  
 DR N-PSDB; AAT33904.  
 XX

PT Nucleic acid encoding human G-protein coupled receptor - for  
 PT diagnosing diseases, and identifying (ant)agonists for asthma and  
 PT allergy treatment

PS Claim 1; Page 55-56; 87pp; English.

CC Novel human G-protein coupled receptor GPR3 (AAM04246) was identified  
 CC as the product of a cDNA clone (AAT33904) isolated from human  
 CC neutrophils. The protein is also expressed in the human liver,  
 CC kidney and pancreas. It shows 39% identity with a known human  
 CC G-protein coupled receptor. Potential ligands include platelet  
 CC activating factor, thrombin, C5a and bradykinin. Recombinant GPR3,  
 CC GPR1, GPR2 and GPR4 (see also AAM04244-45 and AAM04247) can be  
 CC expressed in e.g. E. coli, COS or insect cell hosts for use in  
 CC identifying (ant)agonist cpts. Agonists may be used to treat asthma,  
 CC Parkinson's disease, hypertension, osteoporosis etc., and antagonists  
 CC to treat ulcers, asthma, allergies, etc.

XX Sequence 293 AA;

Query Match 63.5%; Score 1098.5; DB 17; Length 293;  
 Best Local Similarity 76.8%; Pred. No. 9.8e-107;  
 Matches 225; Conservative 14; Mismatches 43; Indels 11; Gaps 4;

QY 1 MNTVMGPFNSERCPDRTRIQVLPALYVVELTGILNTLALMVFHIPSSTFIY 60  
 DB 1 MNTVMGPFNSERCPDRTRIQVLPALYVVELTGILNTLALMVFHIPSSTFIY 60

QY 61 LKNTLVADLIMTLMPKILSDSHLAPMOLRAFCRFSVFEETMYGIVLLGIADR 120  
 DB 61 LKNTLVADLIMTLMPKILSDSHLAPMOLRAFCRFSVFEETMYGIVLLGIADR 120

QY 121 FLKIRPLRNIFLKKPVFAKTVSIFIMFEFISLPNNILSNKEATPSVKKASLKGPL 180  
 DB 121 FLKIRPLRNIFLKKPVFAKTVSIFIMFEFISLPNNILSNKEATPSVKKASLKGPL 180

QY 181 GLKWHQVNNICOPFEWVFTILMLVFYVIAKKYDYSRKSKDRKNNKLEGVFVV 237  
 DB 181 GLKWHQVNNICOPFEWVFTILMLVFYVIAKKYDYSRKSKDRKNNKLEGVFVV 240

QY 238 --VVAVFVCFAPRHFARVPTTHSOTNNKTCRLONOFLIAKETTLFLAAT 287  
 DB 241 LSSICVLHFTS-PEFHITLVKPIRITL--VDCKI-NCLILKKQLSLWQOLT 288

RESULT 14  
 AAB15412  
 ID AAB15412 standard; Protein; 293 AA.

XX AAB15412;  
 XX 17-JAN-2001 (first entry)

DE Human G-protein coupled receptor GRP-3.  
 XX Human; G-protein coupled receptor; GRP-3; 7-transmembrane receptor; ds;  
 KW neutrophil; hybridization probe; diagnostic; tumour; cancer; mutation.  
 XX

XX Homo sapiens.  
 OS  
 XX US6090575-A.

XX 18-JUL-2000.  
 PD 06-JUN-1995; 95US-0467947.  
 XX 30-MAR-1995; 95MO-US04079.

XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX Built CJ, Gentz R, Bult CJ, Sutton GG, Rosen CA, Cao L, Ni J;  
 PI Sutton GG;

XX MPI; 2000-514035/46.  
 DR

DR N-PSDB; AA670770.

XX Polynucleotide encoding a G-protein coupled receptor polypeptide useful  
 PT as a hybridization probe for screening a cDNA library and the  
 PT polypeptide encoded useful for screening antagonist and agonist  
 XX  
 PS Disclosure; Fig 3A-C; 52pp; English.

CC This sequence represents a novel human G-protein coupled receptor 3  
 CC (GRP-3), which is a human 7-transmembrane receptor. The coding sequence  
 CC was isolated from a human neutrophil cDNA library and deposited as ATCC  
 CC 75979. The coding sequence was subcloned into the vector pQE3 for  
 CC expression in bacterial cells and pCDNA1/Amp for expression in COS cells.  
 CC The full length cDNA and a hybridization probe for a cDNA library to isolate  
 CC the full length cDNA and to isolate other cDNAs which have a high  
 CC sequence similarity to the gene or similar biological activity. It is  
 CC also useful for diagnosing by detecting diseases such as tumours and  
 CC cancers or susceptibility to diseases related to presence of mutations  
 CC in the DNA.

XX  
 SQ Sequence 293 AA:

Query Match 63.5%; Score 1098.5; DB 21; Length 293;  
 Best Local Similarity 76.8%; Pred. No. 9.8e-107;  
 Matches 225; Conservative 14; Mismatches 43; Indels 11; Gaps 4;

OY 1 MNTTVAGFNRSECRPRTRIVOLVFPALYTVVFLGILLNTLALMVFPVHSSSTFIY 60  
 DB 1 MNTTVAGFNRSECRPRTRIVOLVFPALYTVVFLGILLNTLALMVFPVHSSSTFIY 60

OY 61 LKNTLVADLIMTLMPFKILSDSHLAPWOLRAFCVCFSSVIEYETMYVGIIVLLGLIAFDR 120  
 DB 61 LKNTLVADLIMTLMPFKILSDSHLAPWOLRAFCVCFSSVIEYETMYVGIIVLLGLIAFDR 120

OY 121 FLKIIRPLRNIFLKKRPVFAKTVSIFWFLFISLPMILSNKEATPSSVKKASIKGPL 180  
 DB 121 FLKIIRPLRNIFLKKRPVFAKTVSIFWFLFISLPMILSNKEATPSSVKKASIKGPL 180

OY 181 GLKHWQNNNICQFIFWYFIIMLVFYVIAKKYVDSYRKSRSKDKNNKLEGGVF--- 237  
 DB 181 GLKHWQNNNICQFIFWYFIIMLVFYVIAKKYVDSYRKSRSKDKNNKLEGGVF--- 237

OY 238 ---VVVAVFVCFAPFHFARVETHSQNNKTDCLONOLFIAKETTLFLAAT 287  
 DB 241 LSSLCVLLHFIS-PEFHILTVKPTIRLT---VDCXI-NCLLKKDLSFWQOLT 288

RESULT 15  
 Y67355  
 AA67355 standard; Protein: 293 AA.

AX AA67355;  
 AC  
 XX 25-APR-2000 (first entry)  
 DT  
 XX  
 DE Human G-protein coupled receptor GPR3 amino acid sequence.  
 XX  
 KW G-protein coupled receptor; GPR3; human; ATCC #75979; tumour; cancer;  
 XX diagnosis.  
 XX Homo sapiens.  
 XX OS  
 XX US5998164-A.  
 XX PN  
 XX 07-DEC-1999.  
 XX PD  
 XX 06-JUN-1995; 95US-0467948.  
 XX PE  
 XX 30-MAR-1995; 95MO-US04079.  
 XX PR  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX PA  
 XX LA Y, Gentz R, Bult CJ, Sutton GG, Rosen CA, Cao L, NI J;  
 PI

XX  
 DR WPI; 2000-125626/11.  
 DR N-PSDB; AA67356.  
 XX  
 PT Genes useful in assays for diagnosing tumours and cancers  
 XX  
 PS Example 3; Fig 3; 51pp; English.

CC This sequence represents a human G-protein coupled receptor GPR3 amino  
 CC acid sequence given ATCC deposit number 75979. The nucleotide sequence  
 CC encoding GPR3 was isolated from human liver, kidney and pancreas. The  
 CC invention relates to G-protein coupled receptor GPR2 (see AA60117)  
 CC which has ATCC number 75976. The GPR2 polypeptide is used as part of a  
 CC diagnostic assay for detecting diseases or susceptibility to diseases  
 CC related to the presence of mutations in the GPR2 polypeptide. Examples  
 CC of the diseases include tumours and cancers related to cell  
 CC transformations. Nucleic acid sequences which specifically hybridise to  
 CC the nucleic acid sequences encoding GPR2 can be used as diagnostic  
 CC probes.

XX  
 SQ Sequence 293 AA:

Query Match 63.5%; Score 1098.5; DB 21; Length 293;  
 Best Local Similarity 76.8%; Pred. No. 9.8e-107;  
 Matches 225; Conservative 14; Mismatches 43; Indels 11; Gaps 4;

OY 1 MNTTVAGFNRSECRPRTRIVOLVFPALYTVVFLGILLNTLALMVFPVHSSSTFIY 60  
 DB 1 MNTTVAGFNRSECRPRTRIVOLVFPALYTVVFLGILLNTLALMVFPVHSSSTFIY 60

OY 61 LKNTLVADLIMTLMPFKILSDSHLAPWOLRAFCVCFSSVIEYETMYVGIIVLLGLIAFDR 120  
 DB 61 LKNTLVADLIMTLMPFKILSDSHLAPWOLRAFCVCFSSVIEYETMYVGIIVLLGLIAFDR 120

OY 121 FLKIIRPLRNIFLKKRPVFAKTVSIFWFLFISLPMILSNKEATPSSVKKASIKGPL 180  
 DB 121 FLKIIRPLRNIFLKKRPVFAKTVSIFWFLFISLPMILSNKEATPSSVKKASIKGPL 180

OY 181 GLKHWQNNNICQFIFWYFIIMLVFYVIAKKYVDSYRKSRSKDKNNKLEGGVF--- 237  
 DB 181 GLKHWQNNNICQFIFWYFIIMLVFYVIAKKYVDSYRKSRSKDKNNKLEGGVF--- 237

OY 238 ---VVVAVFVCFAPFHFARVETHSQNNKTDCLONOLFIAKETTLFLAAT 287  
 DB 241 LSSLCVLLHFIS-PEFHILTVKPTIRLT---VDCXI-NCLLKKDLSFWQOLT 288

Search completed: October 11, 2002, 14:48:41  
 Job time : 35 secs

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On protein - protein search, using sw model

Run on: October 11, 2002, 14:47:00 ; Search time 30 Seconds  
(without alignments)  
1920.244 Million cell updates/sec

File: US-09-924-125-2

Perfect score: 1731  
Sequence: 1 MNTYMOGFNRSEKCPDTR.....KTTASSQENHSSQTDNITLG 333

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: SP-archaea:19:1  
2: SP-bacteria:1  
3: SP-fungi:1  
4: SP-human:1  
5: SP-invertebrate:1  
6: SP-mammal:1  
7: SP-mhc:1  
8: SP-organelle:1  
9: SP-phage:1  
10: SP-plant:1  
11: SP-rodent:1  
12: SP-virus:1  
13: SP-vertebrate:1  
14: SP-unclassified:1  
15: SP-tylous:1  
16: SP-bacteriophage:1  
17: SP-archaeal:1

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1731	100.0	333	4	Q9BPV8
2	1366	78.9	337	11	Q9BD82
3	1128	65.2	228	6	Q9BE53
4	928	48.1	176	4	Q9BY61
5	833	43.6	342	6	Q9SKC3
6	830	47.9	342	6	Q9BGT8
7	829	47.9	342	4	Q9H244
8	813	47.0	342	11	Q9CPV9
9	807	46.6	343	11	Q9EPX4
10	767.5	44.3	338	11	Q9ES56
11	692.5	40.0	358	4	Q9BY21
12	692.5	40.0	358	4	Q9BJ28
13	681.5	39.4	359	11	Q9BXT7
14	541.5	31.3	269	4	Q9BXC2
15	363.5	21.0	367	4	Q9BE21
16	339.5	19.6	337	4	Q9J271

17	337.5	19.5	340	6	Q95N02	Q95N02 sus scrofa
18	331	19.1	342	6	Q9GK76	Q9GK76 capra hircu
19	330.5	19.1	298	4	Q9UD26	Q9UD26 homo sapien
20	325	18.8	342	6	Q9XSD4	Q9XSD4 sus scrofa
21	326	18.8	342	6	Q9RTY5	Q9RTY5 bos taurus
22	320.5	18.5	339	11	Q924T8	Q924T8 rattus norv
23	318.5	18.4	339	11	Q9J471	Q9J471 mus musculu
24	318.5	18.4	352	11	Q99J44	Q99J44 mus musculu
25	315.5	18.2	352	11	Q9JKA7	Q9JKA7 mus musculu
26	310.5	17.9	266	6	Q9RTY6	Q9RTY6 canis fami
27	310.5	17.9	361	11	Q9JJS7	Q9JJS7 mus musculu
28	304.5	17.6	359	11	Q9N0U1	Q9N0U1 ovis aries
29	304	17.5	359	11	Q9EPP3	Q9EPP3 cavia porce
30	303.5	17.5	361	11	Q95811	Q95811 rattus norv
31	302	17.4	377	13	Q98U14	Q98U14 brachydanto
32	301.5	17.4	377	13	Q98U14	Q98U14 pan troglod
33	300	17.3	373	6	Q95LNS	Q95LNS xenopus lae
34	300	17.3	374	13	Q95785	Q95785 macaca fasc
35	298	17.2	380	13	Q9DG06	Q9DG06 meleagris g
36	295.5	17.1	360	6	Q98G77	Q98G77 pan troglod
37	293.5	17.0	361	13	Q9XK57	Q9XK57 xenopus lae
38	293	16.9	400	6	Q95M54	Q95M54 macaca fasc
39	292	16.9	454	4	Q9H573	Q9H573 homo sapien
40	290	16.8	362	11	Q9JL20	Q9JL20 rattus norv
41	290	16.8	362	11	Q9JW10	Q9JW10 mus musculu
42	289.5	16.7	383	13	Q42324	Q42324 calosotomus
43	287	16.6	359	11	Q9EQR9	Q9EQR9 meriones un
44	287	16.6	400	6	Q9MYW9	Q9MYW9 macaca mula
45	286	16.5	393	11	Q9R1M0	Q9R1M0 mus musculu

## ALIGNMENTS

RESULT 1  
ID Q9BPV8 PRELIMINARY: PRT; 333 AA.  
AC Q9BPV8:  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DE PUTATIVE G-PROTEIN-COUPLED RECEPTOR FKSG77 (G-PROTEIN COUPLED RECEPTOR  
DE GPR86) (G-PROTEIN-COUPLED RECEPTOR) (G-PROTEIN-COUPLED RECEPTOR  
DE GPR86)  
GN FKSG77 OR GPR86 OR GPR94.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=HEART;  
RA Wang Y., Gong L.;  
RT "Molecular cloning of FKSG77, a novel gene encoding a putative G-  
RT protein-coupled receptor."  
RL Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.  
[2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21172992; PubMed=11273702;  
RA Wittenberger T., Schaller H.C., Hellebrand S.;  
RT "An expressed sequence tag (est) data mining strategy succeeding in  
RT the discovery of new G-protein coupled receptors."  
RL J. Mol. Biol. 307:799-813(2001).  
[3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21458557; PubMed=11574155;  
RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O.,  
RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;  
RT "Discovery and mapping of ten novel G protein-coupled receptor  
RL genes."  
RL Gene 275:83-91(2001).  
[4]  
RP SEQUENCE FROM N.A.

Query	Subject	Similarity	Score	DB	Length
QY	1 MNTVMQCFNSENSEPCPDTRIVQLVFPALYTVVFTGLINTALVFNHPSSTFIY	78.9%	1366	DB 11	337
Db	5 INTTMOGKNSKSEPCPDTRBMQLFLPVLYVFLAGLINTVLMVFNHPSNSTFIY	77.5%	1316	DB 11	337
QY	61 LKNTVADLIMTMFPFILSDSHLAPQALFVCRFSVYTFEMVYGIYLLGIADR	77.5%	1316	DB 11	337
Db	65 LKNTVADLIMTMFPFILSDSHLAPQALFVCRFSVYTFEMVYGIYLLGIADR	77.5%	1316	DB 11	337
QY	121 FLKIRPLRNFLFKPPVAKTVSIFIPFELFISLPNNILSKKATPSSVKKCAISKPL	77.5%	1316	DB 11	337
Db	125 FLKIRPFRKFEVKKTKNAKTVSISVMSLAFISLPMIL-NKEATPSSVKKCAISKPL	77.5%	1316	DB 11	337
QY	181 GLKHQVANNICQFETMFTILMVFYVIAKVDYSYRSKSDKRNKKLEKRVYVY	77.5%	1316	DB 11	337
Db	184 GLMHQVAVSHCOLFMVAVFIMLEFVAVITKTVNSYRSKRSKSDR-HKRLVYVYVY	77.5%	1316	DB 11	337
QY	241 AVFECFAPFEPFARVPYHNSQANKTDCRLNOLFIKETTFLAATNCMDPLIYILC	77.5%	1316	DB 11	337
Db	243 AVFECFAPFEPFARVPYHNSQANKTDCRLNOLFIKETTFLAATNCMDPLIYILC	77.5%	1316	DB 11	337
QY	301 KKTETKLPQMGKR--TTASSQENNSQTDNITL	77.5%	1316	DB 11	337
Db	303 KKTETKLPQMGKR--TTASSQENNSQTDNITL	77.5%	1316	DB 11	337

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OM protein - protein search, using sw model

Run on: October 11, 2002, 14:48:00 ; Search time 19 seconds  
(without alignments)  
428.091 Million cell updates/sec

Title: US-09-924-125-2

Perfect score: 1731

Sequence: 1 MNTTVQGFNRSEPCPRDTR.....KTTASSQENHSQTDNITIG 333

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued\_Patents\_AA:\*  
1: /cgn2\_6/prodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/5A\_COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/5A\_COMB.pep:\*  
6: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1725	99.7	333	4	US-09-221-456-2
2	1725	99.7	333	4	US-09-558-740-2
3	1697	98.0	333	2	US-08-812-871-1
4	1098.5	63.5	293	2	US-08-467-947A-6
5	1098.5	63.5	293	3	US-08-467-947A-6
6	829	47.9	342	3	US-08-852-824-2
7	777	44.9	325	2	US-08-467-947A-29
8	777	44.9	325	3	US-08-467-947A-29
9	777	44.9	338	4	US-08-852-824-2
10	777	44.9	338	4	US-09-303-524A-2
11	677.5	39.1	358	3	US-08-988-876-3
12	503.5	29.2	319	1	US-08-702-344-28
13	365	21.1	361	1	US-08-383-750-4
14	365	21.1	361	1	US-08-352-678-4
15	365	21.1	361	1	US-08-352-678-4
16	363.5	21.0	339	2	US-08-812-871-3
17	363.5	21.0	339	2	US-08-812-871-3
18	363.5	21.0	339	3	US-09-299-843A-44
19	363.5	21.0	339	4	US-09-088-337B-44
20	363.5	21.0	339	5	PCT-US93-11153-44
21	363.5	21.0	339	5	PCT-US93-07180-2
22	360.5	20.8	381	1	US-08-467-947A-2
23	360.5	20.8	381	1	US-08-467-947A-2
24	360.5	20.8	381	4	US-09-217-101-2
25	359	20.7	348	2	US-08-852-824-17
26	338.5	19.6	347	4	US-09-044-404A-2
27	334.5	19.3	326	1	US-08-118-270-39

#### ALIGNMENTS

28	334.5	19.3	326	5	PCT-US93-08528-39	Sequence 39, App1
29	331.5	19.2	342	3	US-08-988-876-9	Sequence 9, App1
30	300.5	17.4	358	2	US-08-458-970A-11	Sequence 11, App1
31	300	17.3	362	3	US-08-513-974B-374	Sequence 4, App1
32	296	17.1	359	1	US-08-148-209A-4	Sequence 2, App1
33	295	17.0	400	4	US-09-351-198-2	Sequence 2, App1
34	295	17.0	400	4	US-09-113-426-2	Sequence 3, App1
35	292.5	16.9	407	2	US-08-742-440A-3	Sequence 3, App1
36	292	16.9	400	3	US-08-889-108-8	Sequence 8, App1
37	292	16.9	400	4	US-08-188-275A-2	Sequence 8, App1
38	292	16.9	400	5	PCT-US94-10358-8	Sequence 8, App1
39	291	16.8	370	3	US-08-781-250-2	Sequence 2, App1
40	291	16.8	391	2	US-08-454-549-3	Sequence 3, App1
41	291	16.8	391	3	US-08-454-552-3	Sequence 3, App1
42	291	16.8	398	1	US-08-149-093A-5	Sequence 5, App1
43	291	16.8	398	2	US-08-911-245-5	Sequence 5, App1
44	291	16.8	398	3	US-08-889-108-2	Sequence 2, App1
45	291	16.8	398	4	US-08-120-601B-2	Sequence 2, App1

RESULT 1  
US-09-221-456-2  
Sequence 2, Application US/09221456  
Patent No. 6162899  
GENERAL INFORMATION:  
APPLICANT: SATHE, GANESH  
APPLICANT: HALSEY, WENDY  
APPLICANT: MUIR, ALISON  
APPLICANT: CHAMBERS, JON  
TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS  
TITLE OF INVENTION: AND ANTAGONISTS OF THE HREAB1 RECEPTOR  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ratner & Prestlia  
STREET: P.O. Box 980  
CITY: Valley Forge  
STATE: PA  
COUNTRY: USA  
ZIP: 19482  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/221,456  
FILING DATE: 28-DEC-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/956,975  
FILING DATE: 23-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Prestlia, Paul F  
REGISTRATION NUMBER: 23,031  
REFERENCE/DOCKET NUMBER: GH-70318-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-407-0700  
TELEFAX: 610-407-0700  
TELEX: 846169  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 333 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-221-456-2  
Query Match 99.7%, Score 1725, DB 4, Length 333;

Best Local Similarity 99.7%; Pred. No. 1.8e-134;  
Matches 332; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNTVMGSEFNSERCPDRTIVOLVFPALTYVFLTGILNTLALMWVHIPSSTFIY 60  
DB 1 MNTVMGSEFNSERCPDRTIVOLVFPALTYVFLTGILNTLALMWVHIPSSTFIY 60  
QY 61 LKNTLVADLIMTLMPKILSDSHLAPWOLRAFCRSSVIFETMYVGLGLIAFDR 120  
DB 61 LKNTLVADLIMTLMPKILSDSHLAPWOLRAFCRSSVIFETMYVGLGLIAFDR 120  
QY 121 FLKIIIRPLNIFLKPPFAKTVSIFIMFELFISLPNMLISNKEATPSSVKCASLKGPL 180  
DB 121 FLKIIIRPLNIFLKPPFAKTVSIFIMFELFISLPNMLISNKEATPSSVKCASLKGPL 180  
QY 181 GLKHHOVANNICOFIFMTVFILMLVFYVIAKKYDYSRKSKSDRKNKKLEKGFVYV 240  
DB 181 GLKHHOVANNICOFIFMTVFILMLVFYVIAKKYDYSRKSKSDRKNKKLEKGFVYV 240  
QY 241 AVFVCFAPFHFARVPYTHSOTNNKTDCRLONOLFIAKETTLFLAATNICMDPLIYIFLC 300  
DB 241 AVFVCFAPFHFARVPYTHSOTNNKTDCRLONOLFIAKETTLFLAATNICMDPLIYIFLC 300  
QY 301 KKFTEKLPCHMGKRTTASSQENHSSQTDNITLG 333  
DB 301 KKFTEKLPCHMGKRTTASSQENHSSQTDNITLG 333

## RESULT 2

US-09-558-740-2  
Sequence 2, Application US/09558740  
Patent No. 6356695  
GENERAL INFORMATION:  
APPLICANT: SATHE, GANESH  
APPLICANT: HALSEY, WENDY  
APPLICANT: MUIR, ALISON  
APPLICANT: CHAMBERS, JON  
APPLICANT: SZEKERES, PHILIP  
TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND  
FILE REFERENCE: GH-70318-2  
CURRENT APPLICATION NUMBER: US/09/558,740  
CURRENT FILING DATE: 2000-04-26  
PRIOR APPLICATION NUMBER: 08/956,975  
PRIOR FILING DATE: 1997-10-23  
PRIOR APPLICATION NUMBER: 09/221,456  
PRIOR FILING DATE: 1998-12-28  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 333  
TYPE: PRT  
ORGANISM: HOMO SAPIENS  
US-09-558-740-2

Query Match 99.7%; Score 1725; DB 4; Length 333;  
Best Local Similarity 99.7%; Pred. No. 1.8e-134;

Matches 332; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNTVMGSEFNSERCPDRTIVOLVFPALTYVFLTGILNTLALMWVHIPSSTFIY 60  
DB 1 MNTVMGSEFNSERCPDRTIVOLVFPALTYVFLTGILNTLALMWVHIPSSTFIY 60  
QY 61 LKNTLVADLIMTLMPKILSDSHLAPWOLRAFCRSSVIFETMYVGLGLIAFDR 120  
DB 61 LKNTLVADLIMTLMPKILSDSHLAPWOLRAFCRSSVIFETMYVGLGLIAFDR 120  
QY 121 FLKIIIRPLNIFLKPPFAKTVSIFIMFELFISLPNMLISNKEATPSSVKCASLKGPL 180  
DB 121 FLKIIIRPLNIFLKPPFAKTVSIFIMFELFISLPNMLISNKEATPSSVKCASLKGPL 180  
QY 181 GLKHHOVANNICOFIFMTVFILMLVFYVIAKKYDYSRKSKSDRKNKKLEKGFVYV 240  
DB 181 GLKHHOVANNICOFIFMTVFILMLVFYVIAKKYDYSRKSKSDRKNKKLEKGFVYV 240

DB 181 GLKHHOVANNICOFIFMTVFILMLVFYVIAKKYDYSRKSKSDRKNKKLEKGFVYV 240  
QY 241 AVFVCFAPFHFARVPYTHSOTNNKTDCRLONOLFIAKETTLFLAATNICMDPLIYIFLC 300  
DB 241 AVFVCFAPFHFARVPYTHSOTNNKTDCRLONOLFIAKETTLFLAATNICMDPLIYIFLC 300  
QY 301 KKFTEKLPCHMGKRTTASSQENHSSQTDNITLG 333  
DB 301 KKFTEKLPCHMGKRTTASSQENHSSQTDNITLG 333

## RESULT 3

US-08-812-871-1  
Sequence 1, Application US/08812871  
Patent No. 5955303  
GENERAL INFORMATION:  
APPLICANT: Au-Young, Janice  
APPLICANT: Guegler, Kari  
APPLICANT: Muzong, Cheng  
TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr..  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/812,871  
FILING DATE: Filed Herewith  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0237 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 333 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: MMLR3D701  
CLONE: 568987  
US-08-812-871-1

Query Match 98.0%; Score 1697; DB 2; Length 333;  
Best Local Similarity 98.5%; Pred. No. 3.6e-132;

Matches 328; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MNTVMGSEFNSERCPDRTIVOLVFPALTYVFLTGILNTLALMWVHIPSSTFIY 60  
DB 1 MNTVMGSEFNSERCPDRTIVOLVFPALTYVFLTGILNTLALMWVHIPSSTFIY 60  
QY 61 LKNTLVADLIMTLMPKILSDSHLAPWOLRAFCRSSVIFETMYVGLGLIAFDR 120  
DB 61 LKNTLVADLIMTLMPKILSDSHLAPWOLRAFCRSSVIFETMYVGLGLIAFDR 120  
QY 121 FLKIIIRPLNIFLKPPFAKTVSIFIMFELFISLPNMLISNKEATPSSVKCASLKGPL 180  
DB 121 FLKIIIRPLNIFLKPPFAKTVSIFIMFELFISLPNMLISNKEATPSSVKCASLKGPL 180



Db 121 FLKIRPLRNIFLKKPVAKTVSIFIMFLEFISLPNLSNKEATPSSVKCASLKGPL 180  
QY 181 GLKHQWNNNICOFIFMTVFILMLVFYVIAKRYDSYRSKSKDRKNNKLEGVFVV 240  
Db 181 GLKHQWNNNICOFIFMTVFILMLVFYVIAKRYDSYRSKSKDRKNNKLEGVFVV 240  
QY 241 AVFFVCAPFHPARVPYTHSOTNNKTCRLQNLFIKETTLLFLAATNICKDPLIYIFLC 300  
Db 241 PVFFVCAPFHPARVPYTHSOTNNKTCRLQNLFIKETTLLFLAATNICKDPLIYIFLC 300  
QY 301 KKEFEKPCMOGRKTTASSQENHSSQDNDITLG 333  
Db 301 KKEFEKPCMOGRKTTASSQENHSSQDNDITLG 333

RESULT 4  
US-08-467-948A-6  
Sequence 6, Application US/08467948A  
Patent No. 5998164

GENERAL INFORMATION:  
APPLICANT: LI, YI  
APPLICANT: CAO, LIANG  
APPLICANT: NI, JIAN  
APPLICANT: GENTZ, REINER  
APPLICANT: BULT, CAROL J.  
APPLICANT: SUTTON III, GRANGER G.  
APPLICANT: ROSEN, CRAIG A.  
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
TITLE OF INVENTION: Coupled Receptor GPR2  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,948A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04079  
FILING DATE: 30-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: STEFFE, ERIC K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 293 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-467-948A-6

Query Match 63.5%; Score 1098.5; DB 2; Length 293;  
Best Local Similarity 76.8%; Pred. No. 4.2e-83;  
Matches 225; Conservative 14; Mismatches 43; Indels 11; Gaps 4;  
QY 1 MNTTVQGFNRSECRPDRTIVOLVLPALTYVFLGIIILNTALWVFIIPSSSTFIY 60  
Db 1 MNTTVQGFNRSECRPDRTIVOLVLPALTYVFLGIIILNTALWVFIIPSSSTFIY 60  
QY 61 LKNTLVADLIMTLPEFKILSDSHLAPWQLRAFVCRSSVIFETWVGIVLGLIAFDR 120

Db 61 LKNTLVADLIMTLPEFKILSDSHLAPWQLRAFVCRSSVIFETWVGIVLGLIAFDR 120  
QY 121 FLKIRPLRNIFLKKPVAKTVSIFIMFLEFISLPNLSNKEATPSSVKCASLKGPL 180  
Db 121 FLKIRPLRNIFLKKPVAKTVSIFIMFLEFISLPNLSNKEATPSSVKCASLKGPL 180  
QY 181 GLKHQWNNNICOFIFMTVFILMLVFYVIAKRYDSYRSKSKDRKNNKLEGVFVV 240  
Db 181 GLKHQWNNNICOFIFMTVFILMLVFYVIAKRYDSYRSKSKDRKNNKLEGVFVV 240  
QY 238 --VVAVFVCAPFHPARVPYTHSOTNNKTCRLQNLFIKETTLLFLAAT 287  
Db 241 LSLICVLHFTS-PEFHILTVKPTIRLT---VDCKI-NCLILKKQLSWQOLT 288

RESULT 5  
US-08-467-947A-6  
Sequence 6, Application US/08467947A  
Patent No. 6090575

GENERAL INFORMATION:  
APPLICANT: LI, YI  
APPLICANT: CAO, LIANG  
APPLICANT: NI, JIAN  
APPLICANT: GENTZ, REINER  
APPLICANT: BULT, CAROL J.  
APPLICANT: SUTTON III, GRANGER G.  
APPLICANT: ROSEN, CRAIG A.  
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
TITLE OF INVENTION: Coupled Receptor GPR1  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,947A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04079  
FILING DATE: 30-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: STEFFE, ERIC K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 293 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-467-947A-6

Query Match 63.5%; Score 1098.5; DB 3; Length 293;  
Best Local Similarity 76.8%; Pred. No. 4.2e-83;  
Matches 225; Conservative 14; Mismatches 43; Indels 11; Gaps 4;  
QY 1 MNTTVQGFNRSECRPDRTIVOLVLPALTYVFLGIIILNTALWVFIIPSSSTFIY 60  
Db 1 MNTTVQGFNRSECRPDRTIVOLVLPALTYVFLGIIILNTALWVFIIPSSSTFIY 60

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QY      61  LKNTLVADLINTLTLPRKISDSHLAQMOLRAFCRRSSVIFETWVGIVGLGIAFDR  120
Db      61  LKNTLVADLINTLTLPRKISDSHLAQMOLRAFCRRSSVIFETWVGIVGLGIAFDR  120
QY      121  FLKTIIRPLRNIEFLKKPVFAATVSIFIEWFLFEISLPMNLSNKAEATPSYKCAISLGPL  180
Db      121  FLKTIIRPLRNIEFLKKPVFAATVSIFIEWFLFEISLPMNLSNKAEATPSYKCAISLGPL  180
QY      121  FLKTIIRPLRNIEFLKKPVFAATVSIFIEWFLFEISLPMNLSNKAEATPSYKCAISLGPL  180
Db      121  FLKTIIRPLRNIEFLKKPVFAATVSIFIEWFLFEISLPMNLSNKAEATPSYKCAISLGPL  180
QY      181  GLKHKHAWNINICQRIEFTVFIILMVEFVYIYAKKYDSYRKSSEKDRNNKKLEGKYF---  237
Db      181  GLKHKHAWNINICQRIEFTVFIILMVEFVYIYAKKYIMLIESPKYRTEETKTSMAKAYLLSW  240
QY      238  ---VVVAVFVEVCAPFEFAFVAPYTHSQTNNKTCORLONQJIAKETTLFAAT  287
Db      241  LSSLCVLTNHFIS-PEFHILTVVKKPTIRLT---VDCKI-NCILLAKQSLFMQOLT  288

```

## RESULT 6

```

US-08-852-824-2
; Sequence 2, Application US/08852824C
; Patent No. 6060272
; GENERAL INFORMATION:
; APPLICANT: Li et al.
; TITLE OF INVENTION: Human G-Protein Coupled Receptors
; FILE REFERENCE: 1488.122000
; CURRENT APPLICATION NUMBER: US/08/852,824C
; CURRENT FILING DATE: 1997-05-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 342
; TYPE: PRT
; ORGANISM: genomic
US-08-852-824-2

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Query Match	47.9%;	Score 829;	DB 3;	length 342;
Best Local Similarity	49.1%;	Pred. No. 6.5e-61;		
Matches 155;	Conservative 57;	Mismatches 102;	Indels 2;	Gaps 1;

RESULT 7  
US-08-467-948A-29  
; Sequence 29, Application US/08467948A  
; Patent No. 5006154

APPLICANT: BULL, CAROL J.  
 APPLICANT: SUTTON III, GRANGER G.  
 APPLICANT: ROSEN, CRAIG A.  
 TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
 TITLE OF INVENTION: Coupled Receptor GPR2  
 NUMBER OF SEQUENCES: 30  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 STREET: 1100 NEW YORK AVE., NW, SUITE 600  
 CITY: WASHINGTON  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/467,948A  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/04079  
 FILING DATE: 30-MAR-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: STEFFE, ERIC K.  
 REGISTRATION NUMBER: 36,688  
 REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-2540  
 TELEFAX: 202-371-2540  
 INFORMATION FOR SEQ ID NO: 29:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 325 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: not relevant  
 MOLECULE TYPE: peptide  
 US-08-467-948A-29

RESULT 8  
US-08-467-947A-29  
; Sequence 29, Application US/08467947A  
; Patent No. 6090575  
; GENERAL INFORMATION:  
; APPLICANT: LI, YI  
; APPLICANT: CAO, LIANG



```

Patent No. 6238873
GENERAL INFORMATION:
APPLICANT: CHAMBERS, JONATHAN K.
APPLICANT: STEWART, BRIAN R.
APPLICANT: AMES, ROBERT S.
APPLICANT: SARAU, HENRY M.
APPLICANT: FOLEY, JIM
APPLICANT: ARNOLD, ANNE ROMANIC
TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN THE HUMAN KIAA0001
TITLE OF INVENTION: RECEPTOR AND LIGANDS THEREOF
FILE REFERENCE: GP50007
CURRENT APPLICATION NUMBER: US/09/303,524A
CURRENT FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 60/083,957
PRIOR FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 338
TYPE: PRT
ORGANISM: Homo sapiens
US-09-303-524A-2

```

```

Query Match          44.9%; Score 777; DB 4; Length 338;
Best Local Similarity 47.5%; Pred. No. 1.2e-56;
Matches 140; Conservative 54; Mismatches 101; Indels 0; Gaps 0;

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QY 13 EHCPRDTRIVOLVFPALTYVFLGILNTLALWVFIHPSSTFIYIKNTLVADLMT 72
DB 12 EESGONLITOOIIPVLICWFIINGIILNGSVIFVPSKSIYIKNTLVADLMT 71
QY 73 LMLPKIISDSILAWOLARAVCRSSVIFETMVGIVLGLAFDFELKTIPLNITF 132
DB 72 LTFPKIIGDGLGFWOINVPCVSAVLFYVMVSVIFVGLISFDYIYIKVPLMTSF 131
QY 133 LKKPFAVTSIFIFLFFETISLPMIISNKEAPSSVKKCASLKGPIGLMKHGVNNIC 192
DB 132 IQSVSYSLLSVYVIMMLLAVPILITNOSVREYTOIKICHLKSELGRKWHKASNTIF 191
QY 193 QPIETVETILMVEYVIAKVVDSYRSKSKDRKNNKLEGVFVVAVEFCAPPHF 252
DB 192 VAIFIVLLELIVETATIKKIKFSHLSKSRNSTSVKKSRSNIFSIYFVFCVPHI 251
QY 253 ARVPTHSOTNNKTDRCRLQNLFIKETTLLFLAATNICMDPLIYFLCKTEKL 307
DB 252 ARIPYKSTQEAHYSOSKELIRYKTEPLLISANVCLDPLIYFLCOPREIL 306

```

```

RESULT 11
US-08-988-876-3
Sequence 3, Application US/08988876
Patent No. 6063596
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
TITLE OF INVENTION: WITH IMMUNE RESPONSE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

```

```

SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,876
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0441 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSTUT09
CLONE: 1650519
US-08-988-876-3

```

```

Query Match          39.1%; Score 677.5; DB 3; Length 358;
Best Local Similarity 40.7%; Pred. No. 1.8e-48;
Matches 124; Conservative 69; Mismatches 101; Indels 11; Gaps 3;

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```

QY 10 NRSECRDTRIVQ---LVFPALTYVFLGILNTLALWVFIHPSSTFIYIKNTLV 65
DB 25 NRSDEPGKNTLHNEEDTIVLPLILFVASILNGLAWVFIHPSSTFIYIKNTLV 84
QY 66 VADLIMTLMDFKILSDSLAPWOLARAVCRSSVIFETMVGIVLGLAFDFELKTI 125
DB 85 VADLIMTITFPFRIVADGPGWYKFLICRTSVLFYANMTSVIFGLISIDRYKAV 144
QY 126 RPLRNIFLKKVFAKTVSIFIFLFFETISLPMIISNKEAPSSVKKCASLKGPIGLMKH 185
DB 145 KPFSGSRMYSITFTKVLVLSVCWVIAVLSLPNIITNCGPTEDNHDCKSLPLGVKH 204
QY 186 QMNVNICOPIFMTVFIILMVEYVIAKVVDSYRK---SKSDRKNNKLEKVFVVAV 242
DB 205 TAVITYNSCLFVAVALIIGCTIALSKYTHKSSROFISOSKRRKHNSIR---VVAV 260
QY 243 FVFCFAPHFARVPYTHSOTNNKTDRCRLQNLFIKETTLLFLAATNICMDPLIYFLCK 302
DB 261 YFTCFPLPYHLCMPSTFSLDRLDESNOKILYCKEITLFLSACNVCLDPIYFPMGRS 320
QY 303 FTEKL 307
DB 321 FSRWL 325

```

```

RESULT 12
US-08-702-344-28
Sequence 28, Application US/08702344
Patent No. 572315
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: Lavallee, Edward
APPLICANT: Racie, Lisa
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.

```

STREET: 87 Cambridgepark Drive  
 CITY: Cambridge  
 STATE: Massachusetts  
 COUNTRY: U.S.A.  
 ZIP: 02140  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/702,344  
 FILING DATE:  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Brown, Scott A.  
 REGISTRATION NUMBER: 32,724  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 498-8224  
 TELEFAX: (617) 876-5851  
 INFORMATION FOR SEQ ID NO: 28:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 319 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-702-344-28

Query Match 29.2%; Score 505.5; DB 1; Length 319;  
 Best Local Similarity 33.4%; Pred. No. 2.1e-34;  
 Matches 107; Conservative 64; Mismatches 134; Indels 15; Gaps 5;

10 NSERGP--RDRIVGLVLPALTYVFLGILNLTALMVFVHIPSSTFI--YTKTTLV 66  
 3 NSSEFVYKDE---PTTFYFLVGLIGSCFATVAFIKNINRCVSYLLNLT 58  
 67 ADLIMTLMPKILSDSHAPMOLRAFCVRSVIEYETVYGVLLGLAFRPFKIR 126  
 59 ADPLTLALPVIIVDGLVAPMKIKFHCQVTRCLYINMYLIIPLAFVSIDRCLOTH 118  
 127 PLRNLTKLVPFAKTVSIFTFEFLFISLPMNLSNKEATPSSVKKASLKGPLGLKMHQ 186  
 119 SKRIYRQPGKAKMISTYVLMVLLIMVPMNMIPIKDKESNVGCMERKKEFGNMHL 178  
 187 MYNNICQIFMVFILMVFYVIAKVDSTKSKSKDKRNNKLEAKVFAVVAFFVC 246  
 179 LNFICVAFLEFSAIILISNCLVIRQL--YRNKDENVYPNVKKALINILVTGGIIC 235  
 247 FAPFHARVPYTHSOTNNKDCRLQNLFIKETTFLAATNICMDPLIYIFLCKKFTK 306  
 236 FVPIHIVRPIYLSQTEVITDCSTRISLFAKAKETILLAVSNLCFPIILYHLSKAFRSK 295  
 307 LFCMOGRKTTASSQENHSSQ 326  
 296 V-----TETFAFPKRETKAK 310

RESULT 13  
 US-08-383-750-4  
 Sequence 4, Application US/08383750  
 Patent No. 5743301  
 GENERAL INFORMATION:  
 APPLICANT: Birkenbach, Mark  
 APPLICANT: Kieff, Elliot  
 TITLE OF INVENTION: Epstein Barr Virus Induced Genes  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Steiner, Kessler, Goldstein & Fox  
 STREET: 1100 New York Avenue, N.W.,  
 STREET: Suite 600  
 CITY: Washington  
 STATE: D.C.

COUNTRY: U.S.A.  
 ZIP: 20005-3934  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/383,750  
 FILING DATE: Herewith  
 CLASSIFICATION: 436  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fox, Samuel, L.  
 REGISTRATION NUMBER: 30,353  
 REFERENCE/DOCKET NUMBER: 0627.3300001.  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 371-2600  
 TELEFAX: (202) 371-2540  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 361 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 US-08-383-750-4

Query Match 21.1%; Score 365; DB 1; Length 361;  
 Best Local Similarity 27.2%; Pred. No. 8.3e-23;  
 Matches 88; Conservative 78; Mismatches 135; Indels 22; Gaps 7;

23 OLVEPALTYVFLGILNLTALMVFVH---IPSSSTFIYKNTVADLIMTLMPK 78  
 31 RIVMPLKSLVFLIGVNLALVYONKKNIST--LISNVLISDILFTTALPTR 87  
 79 ILSDSHAPMOLRAFCVRSVIEYETVYGVLLGLIARDPLKIRPNILFKKPVF 138  
 88 IAYVAMGDFRIGDGLCALRITVALFYITVAGVNMCTLSIDRFIAVHPLRYKKIRIEH 147  
 139 AKVYSITFELFELFISLPMNI--LSNKEATPSSVKKASLKGPLGLKMHQVNNICOFIF 196  
 148 AKGCIPIVWILVPAQTLPLLINPMSKOEAEIRICMEYPNFEETKSLPW--ILGACFICY 205  
 197 WTEFIMLVYVYVIAKVDSTKSKSKDKRNN--NKTLEGVFAVVAFFVCAPFHARV 255  
 206 VPLIILITICYSQICKLFTKANKPLTERSGVKKALNTIILIVFVLCFTPYHAI 265  
 256 PYTHSQTN--NKTDCRLQNLFIKETTFLAATNICMDPLIYIFLCKKFTK 313  
 266 OHMICKLRFENFLECSGRHSFOISLHFTVCLMNPNCMDPFIIFPACGKRYKRYMLKR 325  
 314 KTAS-----SQENHSSQTD 328  
 326 QVSVSISAVKSAPEENSRREME 348

RESULT 14  
 US-08-352-678-4  
 Sequence 4, Application US/08352678  
 Patent No. 6043351  
 GENERAL INFORMATION:  
 APPLICANT: Birkenbach, Mark  
 APPLICANT: Kieff, Elliot  
 TITLE OF INVENTION: EPSTEIN BARR VIRUS INDUCED GENES  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
 STREET: 600 Atlantic Avenue  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02210  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/352.678
FILING DATE: 30-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/980, 518
FILING DATE: 25-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: B0801/7044
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-352-678-4

```

```

Query Match      21.1%; Score 365; DB 3; Length 361;
Best Local Similarity 27.2%; Pred. No. 8.3e-23;
Matches 88; Conservative 78; Mismatches 135; Indels 22; Gaps 7;

```

```

QY 23 OLVPALTYVFLVGLLNTLALWVH----IPSSFTIYIKNTLVADLMTLMPK 78
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 31 RIVMPLHSLVFIIGLVNGLLVIVONRKINST--LYSTLVISDLFTALPTR 87
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 79 ILSDSLAPWOLRAFCRFSSVIFYETMYVGIIVLGLIAFDRFLIIRPLRNIFLKKPVF 138
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 88 IAYVAMGDFMDRIGDALCRITLALVFYINTYAGVNFMTCLSIDRFLAVHPLRNKIKRIEH 147
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 139 AKTVSIFTFWFLFISLPMNT--LSNKEATPSSVKKCASLKGPLGLKWHQVNNICQPIF 196
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 148 AKGVCIFWILVFAOTLPLLNPMKOEAEIRITCMEYPNFEETKSLPW--ILLGACFIQY 205
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 197 WTVFIMLVFVYVIAKKYVDSYRKSCKDRKN--NKKLEGKVVVAVFVCFAPFHFARV 255
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 206 VPLIILICISQICCKLFRKAKONPLTEKSGVNNKALNTIILIVVFLCTPYHVAII 265
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 256 PYTHSQT--NNKTDCLRONOLFIAKETLLFLAATNICMDPLIYIFLCKKFEKLPQMGGR 313
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 266 QHMIRKLRFNSFLSCSRHSFQISLHFTVCLMNFCCMDPIYFPACGGRKRVNMLKR 325
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   314 KTAS-----SOENHSQTD 328
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 326 QVSVSISAVKSAPENSREMT 348
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 15
PCT-US93-09636-4
Sequence 4, Application PC/TUS9309636
GENERAL INFORMATION:
APPLICANT: Birkendach, Mark
APPLICANT: Kieff, Elliot
TITLE OF INVENTION: Epstein Barr Virus Induced Genes
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

```

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/09636
FILING DATE: herewith
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US93-09636-4

```

```

Query Match      21.1%; Score 365; DB 5; Length 361;
Best Local Similarity 27.2%; Pred. No. 8.3e-23;
Matches 88; Conservative 78; Mismatches 135; Indels 22; Gaps 7;

```

```

QY 23 OLVPALTYVFLVGLLNTLALWVH----IPSSFTIYIKNTLVADLMTLMPK 78
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 31 RIVMPLHSLVFIIGLVNGLLVIVONRKINST--LYSTLVISDLFTALPTR 87
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 79 ILSDSLAPWOLRAFCRFSSVIFYETMYVGIIVLGLIAFDRFLIIRPLRNIFLKKPVF 138
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 88 IAYVAMGDFMDRIGDALCRITLALVFYINTYAGVNFMTCLSIDRFLAVHPLRNKIKRIEH 147
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 139 AKTVSIFTFWFLFISLPMNT--LSNKEATPSSVKKCASLKGPLGLKWHQVNNICQPIF 196
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 148 AKGVCIFWILVFAOTLPLLNPMKOEAEIRITCMEYPNFEETKSLPW--ILLGACFIQY 205
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 197 WTVFIMLVFVYVIAKKYVDSYRKSCKDRKN--NKKLEGKVVVAVFVCFAPFHFARV 255
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 206 VPLIILICISQICCKLFRKAKONPLTEKSGVNNKALNTIILIVVFLCTPYHVAII 265
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 256 PYTHSQT--NNKTDCLRONOLFIAKETLLFLAATNICMDPLIYIFLCKKFEKLPQMGGR 313
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 266 QHMIRKLRFNSFLSCSRHSFQISLHFTVCLMNFCCMDPIYFPACGGRKRVNMLKR 325
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   314 KTAS-----SOENHSQTD 328
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 326 QVSVSISAVKSAPENSREMT 348
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

Search completed: October 11, 2002, 14:50:57
Job time : 20 secs

```

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2002, 14:46:19 ; Search time 13 seconds  
(without alignments)  
991.816 Million cell updates/sec

Title: US-09-924-125-2

Perfect score: 1731

Sequence: 1 MNTVMQGFNRSEKPRDR.....KTTASSQENHSSQTDNITIG 333

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

otal number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	777	44.9	338	1	KI01_HUMAN
2	713	41.2	305	1	KI01_RAT
3	505.5	29.2	319	1	H963_HUMAN
4	392.5	22.7	375	1	GPRY_MOUSE
5	391.5	22.6	381	1	GPRY_MOUSE
6	365	21.1	361	1	EBR2_HUMAN
7	363.5	21.0	339	1	GPRH_HUMAN
8	339.5	19.6	337	1	CLT1_HUMAN
9	337.5	19.5	340	1	CLT1_PIG
10	336.5	19.4	342	1	PAFR_HUMAN
11	331.5	19.2	341	1	PAFR_CAVPO
12	322.5	18.6	342	1	PAFR_RAT
13	320.5	18.5	339	1	CLT1_RAT
14	318.5	18.4	352	1	CLT1_MOUSE
15	315.5	18.2	341	1	PAFR_MOUSE
16	309.5	17.9	359	1	AGZR_BOVIN
17	305.5	17.6	359	1	AGZR_BOVIN
18	303	17.5	362	1	P2R1_MEICA
19	300.5	17.4	359	1	AGZR_HUMAN
20	300	17.3	362	1	P2R1_CHICK
21	299	17.3	359	1	AGZR_CHICK
22	299	17.3	401	1	OPRM_BOVIN
23	298.5	17.2	420	1	THRR_XENLA
24	298	17.2	359	1	AGZR_CANRA
25	297.5	17.2	359	1	AGZR_SHEEP
26	297	17.2	359	1	AGZR_PIG
27	297	17.2	359	1	AGZR_RAT
28	296.5	17.1	308	1	P2R1_CHICK
29	296	17.1	359	1	AGZR_MERIN
30	294.5	17.0	359	1	AGZR_CAVPO
31	293	16.9	359	1	AGZR_MOUSE
32	292.5	16.9	365	1	P2R1_HUMAN
33	292.5	16.9	369	1	PAR3_MOUSE

34	292	16.9	400	1	OPRM_HUMAN	P35372 homo sapien
35	291	16.8	370	1	P2R1_HUMAN	O99677 homo sapien
36	291	16.8	398	1	OPRM_RAT	P33535 ratus norv
37	290.5	16.8	359	1	AG2S_HUMAN	Q13735 homo sapien
38	290.5	16.8	359	1	AG2S_RAT	P29089 ratus norv
39	290	16.8	362	1	RDC1_RAT	O89039 ratus norv
40	289.5	16.7	358	1	IL8B_RABIT	P35344 oryctolagus
41	287	16.6	362	1	RDC1_MOUSE	P56485 mus musculu
42	287	16.6	400	1	OPRM_MACMU	Q95WV9 macaca mula
43	287	16.6	401	1	OPRM_PIG	Q95247 sus scrofa
44	286	16.5	398	1	OPRM_MOUSE	P42866 mus musculu
45	285	16.5	380	1	OPRM_CAVPO	P41144 cavia porce

## ALIGNMENTS

RESULT 1	ID	Sequence	STANDARD	PRT	AA
KI01_HUMAN	1	15-JUL-1998 (Rel. 36, Created)			
AC	Q15391	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)				
DT	30-MAY-2000 (Rel. 39, Last annotation update)				
DE	Probable G protein-coupled receptor KIAA0001.				
GN	KIAA0001				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
OX	NCBI_Taxid=9606;				
RP	SEQUENCE FROM N.A.				
RC	TISUB-Bone marrow;				
RX	MDLINE=96051387; PubMed=7584026;				
RA	Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawabayashi Y.,				
RA	Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;				
RT	"Prediction of the coding sequences of unidentified human genes. I.				
RT	analysis of randomly sampled cDNA clones from human immature myeloid				
RT	cell line KG-1."				
RT	DNA Res. 1:27-35(1994).				
CC	- FUNCTION: ORPHAN RECEPTOR.				
CC	- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
CC	PROBABLE ORTHOLOG OF RAT VTR 15-20.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>				
CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).				
CC	-----				
DR	EMBL: D13626; BAA02791.1;				
DR	GCRDB: GCR_0594;				
DR	InterPro: IPR000276; GPCR_Rhodopsin.				
DR	Pfam: PF00001; 7tm_1; 1.				
DR	PROSITE: PS00237; G-PROTEIN-RECEP_F1.1; FALSE_NEG.				
DR	PROSITE: PS00262; G-PROTEIN-RECEP_F1.2; 1.				
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.				
FT	DOMAIN 1				
FT	TRANSMEM 30				
FT	DOMAIN 51				
FT	TRANSMEM 56				
FT	DOMAIN 77				
FT	TRANSMEM 97				
FT	DOMAIN 118				
FT	TRANSMEM 139				
FT	DOMAIN 160				
FT	TRANSMEM 181				
FT	DOMAIN 209				
FT	TRANSMEM 234				
FT	DOMAIN 255				
FT	TRANSMEM 255				

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FT DOMAIN 256 278 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 279 299 7 (POTENTIAL).
FT DOMAIN 300 338 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 338 AA; 38971 MW; 8DBE/C782CB4753D CRC64;

Query Match 44.9%; Score 777; DB 1; Length 338;
Best Local Similarity 47.5%; Pred. No. 1e-41;
Matches 140; Conservative 54; Mismatches 101; Indels 0; Gaps 0;

OY 13 ERCPDRIVOLVLPALTYVFLGILLNTALWVFIHPSSFTIYLKNTLVADLMT 72
D 12 ESCSQNLLITQOIIIPVLCMFAGIILLNGVSGMIFVPSKSPIIYKLNIVADFWMS 71
OY 73 LMLPKILSDSHLAPWOLRAFCVCRFSVIFETMYVGVLLGLIADFELIIRLRNIF 132
D 72 LTFPKILGSDGLPQWLNLFVCRVSAVLFFVNMVSVIFEGILSFEDRYKIVRPLMTSF 131
OY 133 LKKPVFAKVSIFLWFLFSLPMLISNKEATPSSVSKCA;LKGPIGLKMHQVNNIC 192
D 132 IQSVYSKSLLSVYMWMLLAVPIILITNOSVREVTOIKIHLKSELGRKMHKASNYIF 191
OY 193 QPIFTVYIILVYVYIAKAYDSYRSKSKDRKNKLEGVVAVVAVFVFCAPFHF 252
D 192 VAFIMVYELLIVYATATKIKFISHLKSSRNSTSVKSSRNIFSIYFVFCVFPYHI 251
OY 253 ARVPYTHSTNNKTCRLQNLQFLAKETTLPLAATNICMDPLIYIFLCKRTEKI 307
D 252 ARIPYKQTAHNSCOSKEILRYMKEPTLLSANVCLDPIYFFLQCPRELL 306

RESULT 2
K101_RAT STANDARD; PRT; 305 AA.
ID K101_RAT
AC 035861;
DT 13-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE Probable G protein-coupled receptor VTR 15-20.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Charlton M.E., Williams A.S., Fogliano M., Sweetnam P.M., Duman R.S.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ORPHAN RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC PROBABLE ORTHOLOG OF HUMAN KIAA0001.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U76206; AAB71745.1; -
CC GCRDB; GCR.2520; -
CC InterPro: IPR000276; GPCR_Rhodopsin.
CC Pfam: PF00001; 7tm.1; 1
CC PROSITE: PS00237; G-PROTEIN_RECP_F1_1; FALSE_NEG.
CC PROSITE: PS00264; G-PROTEIN_RECP_F2_1;
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 29 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 30 50 1 (POTENTIAL).
FT DOMAIN 51 55 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 56 76 2 (POTENTIAL).
FT DOMAIN 77 96 EXTRACELLULAR (POTENTIAL).

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FT TRANSEM 97 117 3 (POTENTIAL).
FT DOMAIN 118 139 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 140 160 4 (POTENTIAL).
FT DOMAIN 161 188 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 189 209 5 (POTENTIAL).
FT DOMAIN 210 234 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 235 255 6 (POTENTIAL).
FT DOMAIN 256 278 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 279 299 7 (POTENTIAL).
FT DOMAIN 300 305 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 305 AA; 34800 MW; 640646A6ECC07A3 CRC64;

Query Match 41.2%; Score 713; DB 1; Length 305;
Best Local Similarity 44.4%; Pred. No. 8.6e-38;
Matches 130; Conservative 57; Mismatches 104; Indels 2; Gaps 1;

OY 2 NTVVQGFNRSERCPRDRIYOLVLPALTYVFLGILLNTALWVFIHPSSFTIYL 61
D 3 NNTTTE--PPKPCRNLLITQOIIIPMLICYVFTIGVLLNGISGMIFVPSKSPIIYL 60
OY 62 KNTLVADLINTLMPKILSDSHLAPWOLRAFCVCRFSVIFETMYVGVLLGLIADFRE 121
D 61 KNTLVADLIMGLTFEPFKVLSGGLPQWLNLFVCRVSAVLFFVNMVSVIAFGLISFDYR 120
OY 122 LKTIIRPLNIFLKKPVFAKVSIFLWFLFSLPMLISNKEATPSSVSKCA;LKGPIGL 181
D 121 KYIKPPLVSVTQSVNYSKIVSLVWVLMLLAVPIILITNOSVQVDVNIQCMELKNEIG 180
OY 182 LKMHQVNNICQFIETVYIILVYVYIAKAYDSYRSKSKDRKNKLEGVVAVVAVV 241
D 181 RKMVKASNYVVSIFMIVYFLLTYFYNAITRKIFSHLSKRNSTSVKSSRNIFSIYL 240
OY 242 VFCVFCAPFHFARVPYTHSTNNKTCRLQNLQFLAKETTLPLAATNICMDPL 294
D 241 AVFACFAPYHVARIPYTHSTNNKTCRLQNLQFLAKETTLPLAATNICMDPL 293

RESULT 3
H963_HUMAN STANDARD; PRT; 319 AA.
ID H963_HUMAN
AC 014626;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Probable G protein-coupled receptor H963.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue-Peripheral blood monocytes;
RC MEDLINE=98036061; Pubmed=9370294;
RA Jacobs K.A., Collins-Racie L.A., Colbert M., Duckett M.,
RA Jacobs-Fleet M., Kelleher K., Kitz R., Lavallee E.R., Merberg D.,
RA Spaulding V., Stover J., Williamson M.D., McCoy J.M.;
RT "A genetic selection for isolating cDNAs encoding secreted proteins."
RL Gene 198;289-296(1997).
CC -1- FUNCTION: ORPHAN RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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DR EMBL: AF002986; AAC51846.1;
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 21
FT TRANSSEM 22 42
FT TRANSSEM 43 48
FT TRANSSEM 49 69
FT TRANSSEM 70 89
FT TRANSSEM 90 110
FT TRANSSEM 111 132
FT TRANSSEM 133 153
FT TRANSSEM 154 181
FT TRANSSEM 182 202
FT TRANSSEM 203 224
FT TRANSSEM 225 245
FT TRANSSEM 246 268
FT TRANSSEM 269 289
FT TRANSSEM 290 319
FT DOMAIN 3 3
FT CARBOHYD 3
SQ SEQUENCE 319 AA; 36754 MW; 79B9821C10841114 CRC64;

Query Match
Best Local Similarity 29.2%; Score 505.5; DB 1; Length 319;
Matches 107; Conservative 64; Mismatches 134; Indels 15; Gaps 5;

QY 10 NNSERP--RDRIVOLVPALTYVFLGILNTLALWVFIHPSSTFI-ILKNTLV 66
DB 3 NSSEFCBPVVKDLE---PTFFYFLVFLVGIISCFATMAFIQKNTNHCVCSTILNLT 58
QY 67 ADILITLMPEKILSHAPQMLRAFCVSSVIFETNYGVILGLAFDRFLKIR 126
DB 59 ADPLTLALPVKIVDLGVAPMKLIFHCVCVACLIIYNNYLIIFLAFVSDRCOLTH 118
QY 127 PLRNIFLKRVPKAVTSIFWFLFISLPNMLISNKEATPSSVKKCASGLPKLKHQ 166
DB 119 SKIRVIOEPGFAKMLSTVWMLVLLIMPMNMIPIKDIKEKSNVCGMEKKEGRMHL 178
QY 187 MYNNICQIFFTVFILMLVYVVIKAYVDYKRSKSKRKNKKLEGVVAVVAVFVC 246
DB 179 LNFICVALFELNFSAILISNCVIRQL--YNNKDNENYPNVKALINLLVTTGIIIC 235
QY 247 FAPFHRVRYHSCQNNNTDCLQNLQFLAKETTLFLAATNCDPLIYFLCKKFTK 306
DB 236 FVPYHVRIPYLSQEVITDCSTRISLTKAKAEATLLAVSNLCFDFILYHLSKAFRSK 295
QY 307 LPCMOGRKTTASSQENHSQ 326
DB 296 V-----TERFASPKERKAK 310

RESULT 4
ID GPRY_MOUSE STANDARD; PRI: 375 AA;
AC 09RIK6;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Probable G protein-coupled receptor GPR34.
GN GPR34.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RA MEDLINE=99326137; PubMed=10395919;
RA Schöneberg T., Schulz A., Grosse R., Schade R., Henkels P.,
RA Schultz G., Gudermann T.;
RT "A novel subgroup of class I G-protein-coupled receptors.";
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RL Blochim. Biophys. Acta 1446:57-70(1999).
CC -1- FUNCTION: ORPHAN RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- TISSUE SPECIFICITY: BROADLY EXPRESSED.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL: AF081916; AAD50550.2;
DR MGI: 134634; Gpr34.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor; G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 54
FT TRANSSEM 55 75
FT TRANSSEM 76 81
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FT TRANSSEM 103 121
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FT TRANS
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CC -1- TISSUE SPECIFICITY: B-LYMPHOCYTE CELL LINES.
CC -1- INDUCTION: BY EBV.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-5 IS THE INITIATOR.
-----
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CC or send an email to license@isb-sib.ch).
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DR DRL EMBL: L08177; AAA35924.1; -
DR DR PIR: B45680; B45680.
DR DR GCRRdb: GCR_0499; -
DR DR MIM: 605741; -
DR DR InterPro: IPR000276; GPCR_Rhodopsn.
DR DR Pfam: PF00001; 7tm_1; 1.
DR DR PRINTS: PRO0237; GPCRRHODOPSN.
DR DR PROSITE: PS00237; G-PROTEIN_RECEP_F1.1; 1.
DR DR PROSITE: PS00262; G-PROTEIN_RECEP_F1.2; 1.
KM KM G-protein coupled receptor; Transmembrane; Glycoprotein.
FT FT DOMAIN 1 31
FT FT TRANSMEM 32 57
FT FT DOMAIN 58 77
FT FT TRANSMEM 78 95
FT FT DOMAIN 96 105
FT FT TRANSMEM 106 127
FT FT DOMAIN 128 149
FT FT TRANSMEM 150 168
FT FT DOMAIN 169 192
FT FT TRANSMEM 193 215
FT FT DOMAIN 216 241
FT FT TRANSMEM 242 265
FT FT DOMAIN 266 287
FT FT TRANSMEM 288 312
FT FT DOMAIN 313 361
FT FT DOMAIN 361 412
FT FT DISULFID 104 181
FT FT SEQUENCE 361 AA; 41224 MM; BSA2171F34C9C67B CRC64;
Query Match 21.18; Score 365; DB 1; Length 361;
Best Local Similarity 27.28; Pred. No. 3e-16;
Matches 88; Conservative 78; Mismatches 135; Indels 22; Gaps 7;
QY 23 QLVPAATVVEFLGILLNTLALWVH---ISSSFIIYLKNTLVADLIMLMPEK 78
Db 31 RIVMDLAHSLEVFITGLVNLTALVAYONRKRIINST--LYSTNLVASDILFTLTPTR 87
QY 79 ILSDSHLAPMOLAFVCFSSVIFYETWVGIVVLGLIAFRFLKIHLPLNIPLKKPVF 138
Db 88 IAYAMGDMDMGALCALCRITALVFIINTYAGVNMTCISLDIFAAVNHPLRYNKIKIEH 147
QY 139 AKTVSIETWEFLFELISPNMI--LSNRKAPSSVYKCAASLKGPIGLKHOMVNNICOFIF 196
Db 148 AKGVCIEMWIIIVEQTLPFLILNPMSKOEAERITCMEXPNEFEKSLPM--ILGACITGY 205
QY 197 WTVFILMVFFVYAKKYVDYSRKSCKDRKN-NKILEGVVVVAVFYFCAPFHRAVY 255
Db 206 VLPILITICTSQICKLFRAKNOMPLETEKSGVKKALNTIILIIVYVLCFEPYHAII 265
QY 256 PYTHSQT--NNKTQCRLONOLELIKETTLLFLAANICMODPIYFIELCKFKTEKLPCMOGR 313
Db 266 QHMINKLRFSNFLECSQRHSFOJLSHTTVCMLAMPNCMDPFITTFACKGKRKVMRLKR 325
QY 314 KTAS-----SQENHSQTD 328
Db 326 QVSVISAAVSKADENSREMT 348
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ID	GPRL_HUMAN	STANDARD:	PRT:	339 AA.
AC	013304:			
DT	01-NOV-1997	(Rel. 35, Created)		
DT	01-NOV-1997	(Rel. 35, Last sequence update)		
DT	16-OCT-2001	(Rel. 40, Last annotation update)		
DE	Putative G protein-coupled receptor GPRL7 (R12).			
GN	GPRL7.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID:9606;			
RA	SEQUENCE FROM N.A.			
RA	MEDLINE:96145150; PubMed:8558062;			
RA	Report C.J., Schweickart V.L., Chantry D., Eddy R.L. Jr., Shows T.B.,			
RA	Godiska R., Gray P.W.;			
RT	"New members of the chemokine receptor gene family.";			
RL	J. Leukoc. Biol. 59:18-23(1996).			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE:96145150; PubMed:8558062;			
RP	Report C.J., Schweickart V.L., Chantry D., Eddy R.L. Jr., Shows T.B.,			
RP	Godiska R., Gray P.W.;			
RP	"New members of the chemokine receptor gene family.";			
RP	J. Leukoc. Biol. 59:18-23(1996).			
RP	SEQUENCE FROM N.A.			
RP	TISSUE-Hippocampus;			
RP	MEDLINE:98181695; PubMed:9523551;			
RP	Blaesius R.H., Weber R.G., Lichter P., Ogilvie A.;			
RP	"A novel orphan G protein-coupled receptor primarily expressed in the			
RP	brain is localized on human chromosomal band 2q21.";			
RP	J. Neurochem. 70:1357-1365(1998).			
RP	-1- FUNCTION: ORPHAN RECEPTOR. POTENTIAL CHEMOKINE RECEPTOR.			
RP	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
RP	-1- TISSUE SPECIFICITY: PRIMARILY EXPRESSED IN BRAIN.			
RP	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
RP	-----			
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RP	modified and this statement is not removed. Usage by and for commercial			
RP	entities requires a license agreement (See <a href="http://www.isb.ch/announce/">http://www.isb.ch/announce/</a>			
RP	or send an email to <a href="mailto:license@isb.slb.ch">license@isb.slb.ch</a> ).			
RP	-----			
RP	EMBL: U33447; AAB16746.1; -			
RP	EMBL: Z94154; CAB08107.1; -			
RP	HSSP: P34996; IDDD.			
RP	GCRdb: GCR_1968; -			
RP	GCRdb: GCR_2597; -			
RP	MIM: 603071; -			
RP	InterPro: IPR000276; GPCR_Rhodpsn.			
RP	Pfam: PF00001; 7tm_1; 1.			
RP	PRINTS: PR00237; GPCRHOPOSN.			
RP	DR PROSITE: PS00237; G-PROTEIN_RECPE_F1_1; 1.			
RP	DR PROSITE: PS50262; G-PROTEIN_RECPE_F1_2; 1.			
RP	KW G-Protein coupled receptor; Transmembrane; Glycoprotein.			
RP	FT DOMAIN 1 36			
RP	FT TRANSSEM 37 57			
RP	FT DOMAIN 58 64			
RP	FT TRANSSEM 65 85			
RP	FT DOMAIN 86 105			
RP	FT TRANSSEM 106 126			
RP	FT DOMAIN 127 147			
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RP	FT CARBOHYD 14 14			
RP	FT CARBOHYD 176 176			
RP	FT CARBOHYD 254 254			
RP	SEQUENCE 339 AA; 37826 MW; BD2AEDB2FEF15E1 CRC64;			

Query Match

21.0%; Score 363.5; DB 1; Length 339;

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CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- TISSUE SPECIFICITY: Widely expressed, with highest levels in spleen and peripheral blood leukocytes. Lower expression in several tissues, such as lung (mostly in smooth muscle bundles and alveolar macrophages), placenta, small intestine, pancreas, colon and heart...
CC -I- MISCELLANEOUS: Selective antagonists, such as montelukast (Singulair), zafirlukast (Accolate) and pranlukast (Onon), are used in the treatment of the asthma crisis.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; AF119711; AAD4285.1; -
DR EMBL; AF133266; AAD42778.1; -
DR MIM; 300201; -
DR HSSP; P34966; 1DDJ.
DR InterPro: IPR004071; CysLeuk_receptor.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PRO1533; CYSTRRECPR.
DR PRINTS; PR00237; GPCRRHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; FALSE_NEG.
DR PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW G-Protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 28
FT TRANSMEM 29 49
FT DOMAIN 50 57
FT TRANSMEM 58 78
FT DOMAIN 79 106
FT TRANSMEM 107 127
FT DOMAIN 128 141
FT TRANSMEM 142 162
FT DOMAIN 163 193
FT TRANSMEM 194 214
FT DOMAIN 215 230
FT TRANSMEM 231 251
FT DOMAIN 252 276
FT TRANSMEM 277 297
FT DOMAIN 298 337
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FT CARBOHYD 169 169
FT CARBOHYD 180 180
FT CARBOHYD 262 262
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Best local similarity 29.8%; Pred. No. 1,je-14;
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Db 25 YSTLYTMSIVYGFGNGFVLVYLVIKTGHHKKSARDVVYNINLAVDLLCVLPRLRVYYV 84

OY 84 HLAQMOLRAFCRCRSSVYFETMGVGYLGGLIAFDRLKIIRPLRNIFLKRPFAKYVS 143
   |:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 85 HKGIWLRGDFGLCRISTAYALVNLVCISIFEFMAEFSFRICAIIVFPVONINTORKAREVC 144

QY 144 IFINFLEFFELIPNNIIISNKKEATPPSVKCAASGLPGILCKHOW-NNICOFI-FWTVEI 201
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Db 145 VGMIIEFVLISSP-FLNAKPDKDEKNNTKCCEPPQDNQTKNHVLYLVHSLSFGFIIPFY 203

OY 202 LMLVYVYVIAAKVYDSTRKSKSDRKRNKKIKEGVYVVAVFVCEAPFHVARVPYTHSQ 261
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Db 204 IIIVCYMI---ILTLLKSKMKRMISSHKRIIGIMIVTTAAFLVSLFMPYHIOTFIHLFL 260
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QY 262 TNKTD- R1N0LFIANKETTLFLAATNICMDPLIYIFLCKKFEKLPOMGRKTTA 317  
 DB 261 HNEKPCDSVLRMQKSVYI-----TLSLAASNCPCDPLIYFSGGFRRLSTF--RKHS 314  
 QY 318 SS 319  
 DB 315 SS 316

RESULT 9  
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 AC 095N02;  
 DT 01-MAR-2002 (Rel. 41, Created)  
 DT 01-MAR-2002 (Rel. 41, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Cysteinyl leukotriene receptor 1 (cysltr1).  
 GN CysLTR1 OR CysLT1.  
 OS Sus scrofa (Pig).  
 C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.  
 NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Takasaki J., Kamohara M., Saito T., Matsumoto M., Matsumoto S.,  
 RA Ohishi T., Soga T., Matsushima H., Furuchi K.;  
 RT "Characterization of cloned rat and porcine cysteinyl leukotriene  
 RT receptors.";  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Receptor for cysteinyl leukotrienes mediating  
 CC constriction of the microvascular smooth muscle during an  
 CC inflammatory response. This response is mediated via a G-protein  
 CC that activates a phosphatidylinositol-calcium second messenger  
 CC system (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: AB052686, BAB60826.1;  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PROSITE: PS00237; G-PROTEIN\_RECEP\_F1.1; FALSE\_NEG.  
 DR PROSITE: PS00262; G-PROTEIN\_RECEP\_F1.2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 31  
 FT TRANSMEM 32 52  
 FT DOMAIN 53 60  
 FT TRANSMEM 61 81  
 FT DOMAIN 82 109  
 FT TRANSMEM 110 130  
 FT DOMAIN 131 144  
 FT TRANSMEM 145 165  
 FT DOMAIN 166 196  
 FT TRANSMEM 197 217  
 FT TRANSMEM 218 233  
 FT TRANSMEM 234 254  
 FT TRANSMEM 255 279  
 FT TRANSMEM 280 300  
 FT DOMAIN 301 340  
 FT DISULFID 340 340  
 FT BY SIMILARITY.  
 FT CARBOHYD 6 6  
 FT CARBOHYD 18 18  
 FT CARBOHYD 172 172  
 FT CARBOHYD 265 265  
 FT CARBOHYD 340 AA; 38986 MW; 54F9372A121CE413 CRC64;  
 SQ SEQUENCE

Query Match 19.5%; Score 337.5; DB 1; Length 340;  
 Best Local Similarity 29.4%; Pred. No. 1,4e-14;  
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 QY 25 VEPALYVVFVFLGILLNLAWEVH-IPSSSTFIYKNTLVADLITMLPKRISDS 83  
 DB 28 VYSLTSMITVVFPGNGFVLYVLTKEKSNQVYVIMINAVDLQVCLPLRVIYV 87  
 QY 84 HLPWOLRAFYCRFSVYIEFTMYGIVLGLIAEDRFLKIRPLRNIFLKRPFAKVS 143  
 DB 88 HKGIWLFEGDFLCRLSTVLYVNLVCSIFPMTAMSFRCIALVFPVONLITHKAKIYC 147  
 QY 144 IEIFEFLFISLPMILSNKRAEIPSSVAKKSLGIPGLKHHQWV-NNICOFI-FWYVFI 201  
 DB 148 IAIWLFVLTSSP-FLMSTSYKDEKNKCEPPOXQAKHVLVLYHVSLEVGFIIPFV 206  
 QY 202 LALVEYVYIAKRVDSYKSKDRKNNKLEGVVAVFVCFAPFHFARVPYHSQ 261  
 DB 207 IIVCYTMI---ILTLKNSKKNNISKKRAIGMIYVTAFLISFMPYRIQRIHLHL 263  
 QY 262 TNKTD- R1N0LFIANKETTLFLAATNICMDPLIYIFLCKKFEKLPOMGRKTTA 317  
 DB 264 HNDYKHCDSVLRMQKSVYI-----TLSLAASNCPCDPLIYFSGGFRREG 309  
 QY 318 SSQENHSQT 327  
 DB 310 STFRKHSIST 319

RESULT 10  
 PAFR\_HUMAN STANDARD; PRT; 342 AA.  
 AC P25105;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Platelet activating factor receptor (PAF-R).  
 GN PAFR OR PAFR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-92028922; PubMed-1656963;  
 RA Ye R.D., Prossnitz E.R., Zou A., Cochrane C.G.;  
 RT "Characterization of a human cDNA that encodes a functional receptor  
 RT for platelet activating factor";  
 RL Biochem. Biophys. Res. Commun. 180:105-111(1991).  
 RP [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Leukocyte;  
 RX MEDLINE-92041873; PubMed-1657923;  
 RA Nakamura M., Honda Z., Izumi T., Sakanaka C., Mutoh H., Minami M.,  
 RA Bito H., Seyama Y., Matsumoto T., Noma M., Shimizu T.;  
 RT "Molecular cloning and expression of platelet-activating factor  
 RT receptor from human leukocytes";  
 RL J. Biol. Chem. 266:20400-20405(1991).  
 RP [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-92250505; PubMed-1374385;  
 RA Kunz D., Gerard N.P., Gerard C.;  
 RT "The human leukocyte platelet-activating factor receptor. cDNA  
 RT cloning, cell surface expression, and construction of a novel  
 RT epitope-bearing analog";  
 RL J. Biol. Chem. 267:9101-9106(1992).  
 RP [4]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-92347886; PubMed-1322356;  
 RA Seyfried C.E., Schweickart V.L., Godiska R., Gray P.W.;  
 RT "The human platelet-activating factor receptor gene (PAFR) contains  
 RT no introns and maps to chromosome 1";  
 RL Genomics 13:832-834(1992).

RN [5] SEQUENCE FROM N.A.  
 RP TISSUE-Heart;  
 RC MEDLINE-93112021; PubMed-1281995;  
 RA Sugimoto T., Tsuchimochi H., McGregor C.G., Mutch H., Shimizu T.,  
 RA Kuwachi Y.;  
 RT "Molecular cloning and characterization of the platelet-activating  
 RT factor receptor gene expressed in the human heart."  
 RL Biochem. Biophys. Res. Commun. 189:617-624(1992).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Behal R.H., Debussche M.S., Olson M.S.;  
 RL Submitted (xxx-1992) to the EMBL/Genbank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-93192035; PubMed-8383507;  
 RA Chase P.B., Halonen M., Regan J.W.;  
 RT "Cloning of a human platelet-activating factor receptor gene:  
 RT evidence for an intron in the 5'-untranslated region."  
 RL Am. J. Respir. Cell Mol. Biol. 8:240-244(1993).  
 CC -1- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC  
 CC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-  
 CC MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDATE ITS  
 CC ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-  
 CC CALCIUM SECOND MESSENGER SYSTEM.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC -----  
 DR EMBL; M80436; AAA60001.1; -  
 DR EMBL; M76674; AAA60002.1; -  
 DR EMBL; D10202; BAA01050.1; -  
 DR EMBL; M88177; AAA60214.1; -  
 DR EMBL; S52624; AAB24695.2; -  
 DR EMBL; L07334; AAB60108.1; -  
 DR EMBL; S56396; AAB25755.1; -  
 DR PIR; JH0479; JH0479.  
 DR PIR; A40191; A40191.  
 DR PIR; A41079; A41079.  
 DR GCRDB; GCR 0186; -  
 DR GCRDB; GCR 0260; -  
 DR GCRDB; GCR 0285; -  
 DR GCRDB; GCR 0414; -  
 DR GCRDB; GCR 0478; -  
 DR GCRDB; GCR 0548; -  
 DR GCRDB; GCR 0731; -  
 DR MIM; 173393; -  
 DR InterPro; IPR000276; GPCR\_Rhodopsin.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PRO1153; PAFRECEPTOR.  
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.  
 DR PROSITE; PS50262; G-PROTEIN RECEPTOR FL 2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Chemotaxis;  
 KW Polymorphism.  
 FT DOMAIN 1 16 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 17 38 1 (POTENTIAL).  
 FT DOMAIN 39 54 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 55 74 2 (POTENTIAL).  
 FT DOMAIN 75 91 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 92 113 3 (POTENTIAL).  
 FT DOMAIN 114 133 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 134 155 4 (POTENTIAL).  
 FT DOMAIN 156 184 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 185 205 5 (POTENTIAL).  
 FT DOMAIN 206 233 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 234 254 6 (POTENTIAL).

FT DOMAIN 255 276 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 277 296 7 (POTENTIAL).  
 FT DOMAIN 297 342 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 90 173 BY SIMILARITY.  
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARIANT 224 224 A->D (IN DBSNP:5938).  
 FT VARIANT 224 224 /FTID-VAR\_011851.  
 FT VARIANT 338 338 N->S (IN DBSNP:5939).  
 FT VARIANT 338 338 /FTID-VAR\_011852.  
 FT CONFLICT 28 28 L->P (IN REF. 6).  
 FT CONFLICT 66 66 F->L (IN REF. 6).  
 FT CONFLICT 95 95 C->R (IN REF. 6).  
 FT CONFLICT 227 228 KR->TG (IN REF. 4).  
 FT CONFLICT 227 228 KR->TT (IN REF. 6).  
 FT CONFLICT 247 247 P->A (IN REF. 6).  
 FT CONFLICT 316 316 K->N (IN REF. 5).  
 SQ SEQUENCE 342 AA; 39203 MW; 890073C95BA79228 CRC64;  
 Query Match 19.48; Score 336.5; DB 1; Length 342;  
 Best Local Similarity 26.28; Pred. No. 1.66-14;  
 Matches 87; Conservative 75; Mismatches 137; Indels 33; Gaps 9;  
 QY 18 DTRIVOLFPALVYVFLGILNTLALVFNHPSSTF---IYLNNTLVADILMTLM 74  
 DB 10 DSEFRYTLFPYVSIIFVIGVANGVYLVAFARLYPCCKFKFNINLVNMDMLPLIT 69  
 QY 75 LPFKLSHLAPQQLAFVGRFSVIEYEMVGVIVLGLAFRFLKIRPLANIFLK 134  
 DB 70 LPLMTVYQNOGNMFLPFLCNVAGCLFINTYCSVAELGVITTRFOAVTRPITAOAN 129  
 QY 135 KPVAKTVSIWFELFISLPMILSNKEATPS---YKCAS--LKGPLGKWHOM 187  
 DB 130 TRKGISLSLVIAVAIVAGASYFLIDSTNVDPBAGSGNTVRCHEHKEKSVPR--LI 186  
 QY 188 VNNICQFETVFTLMVYVIAKYDYRSKSKDKRNNKLEGR---VEVVAVF 243  
 DB 187 IHIFVSFFLVFLIFLCNVLIITRL---MQPVQOQRNAEYKRRLMMVCTVLAVF 241  
 QY 244 FVCFAPFARFAPVPTHSGTNNKTCRLONOLFIKETTLFLATNICHMDPLIYIFLCKKF 303  
 DB 242 IICFVPHVQLPWTLLELGRQ-DSKFRQALINDAQVTLCLSTNCVDPVYICPLTKRF 300  
 QY 304 ---TEKLPQMGGRKTRASSQENHSSQTDNIT 331  
 DB 301 RKHLTEKFSNR-----SSRCKSRATDVT 326  
 RESULT 11  
 PAFR\_CAVPO  
 ID PAFR\_CAVPO STANDARD; PRT; 342 AA.  
 AC P21556;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Platelet activating factor receptor (PAF-R).  
 GN PAFR.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriognathu; Caviidae; Cavia.  
 OX NCBI\_TaxID-10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP TISSUE-Lung;  
 RC MEDLINE-91101726; PubMed-1846231;  
 RX Honda Z.-I., Nakamura M., Miki I., Minami M., Watanabe T., Seyama Y.,  
 RA Okada H., Toh H., Ito K., Miyamoto T., Shimizu T.;  
 RT "Cloning by functional expression of platelet-activating factor  
 RT receptor from guinea-pig lung."  
 RL Nature 349:342-346(1991).  
 CC -1- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC  
 CC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-  
 CC MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDATE ITS  
 CC ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL.



[illegible]

RT "Molecular cloning and functional characterization of murine  
RT cysteinyl-leukotriene 1 (CysLT1) receptors.";  
RL Biochem. Pharmacol. 62:1193-1200(2001).  
RN [3]





DR	EMBL; D50872; BAA09468.1; -	
DR	GCDDB; GCR_1618; -	
DR	MGI; MGI:106066; Pfaff.	
DR	InterPro; IPR000276; GPCR_Rhodpsn.	
DR	Pfam; PF00001; 7tm.1; 1.	
DR	PRINTS; PR01153; PAFRECEPTOR.	
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.	
DR	PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.	
KM	G-protein coupled receptor; Transmembrane; Glycoprotein; Chemotaxis.	
KM		
FT	DOMAIN	1 16
FT	TRANSMEM	17 38
FT	DOMAIN	39 54
FT	TRANSMEM	55 74
FT	DOMAIN	75 91
FT	TRANSMEM	92 113
FT	DOMAIN	114 133
FT	TRANSMEM	134 155
FT	DOMAIN	156 184
FT	TRANSMEM	185 205
FT	DOMAIN	206 233
FT	TRANSMEM	234 254
FT	DOMAIN	255 275
FT	TRANSMEM	276 295
FT	DOMAIN	296 341
FT	CARBOHYD	4 4
FT	CARBOHYD	169 169
FT	DISULFID	90 113
SQ	SEQUENCE	341 AA: 39148 MW: 39148 MW: CAAC8DBDBD26897 CRC64;

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OW protein - protein search, using sw model

Run on: October 11, 2002, 14:47:34 ; Search time 23 Seconds

(without alignments)  
1391.206 Million cell updates/sec

Title: US-09-924-125-2

Perfect score: 1731

Sequence: 1 NMTVTWQGNRSEHRCPRDTR.....KTTASSQENHSSQTDVITIG 333

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

otal number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR\_71:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	365	21.1	361	2	B45680
2	336.5	19.4	342	2	A40191
3	331.5	19.2	342	2	S13638
4	322.5	18.6	341	2	S43252
5	315.5	18.2	341	2	S63666
6	309.5	17.9	359	2	S15403
7	305.5	17.6	359	2	A48857
8	300.5	17.4	359	2	JC1104
9	300	17.3	362	2	S33733
10	300	17.3	373	2	JEO087
11	299	17.3	359	2	JH0621
12	298.5	17.2	420	2	I51667
13	297	17.2	359	2	S44425
14	296.5	17.1	359	2	JC2134
15	296.5	17.1	368	2	I50241
16	293.5	16.9	305	2	S68679
17	292	16.9	370	2	JC5549
18	292	16.9	392	2	S65693
19	292	16.9	400	2	I56553
20	291	16.8	398	2	I56517
21	290.5	16.8	359	2	A46566
22	290.5	16.8	359	2	I39418
23	289.5	16.7	358	2	A53752
24	286	16.5	359	2	JC1194
25	286	16.5	398	2	A57510
26	285.5	16.5	359	2	JQ1516
27	285	16.4	380	2	A55259
28	284	16.4	373	2	JC4737
29	284	16.4	380	2	JC3338

30	283.5	16.4	344	2	T09508	Inton 17 purinerg
31	283.5	16.4	360	2	G02064	G protein-coupled
32	283.5	16.4	380	2	I38435	angiotensin recept
33	283	16.3	362	2	A39714	G protein-coupled
34	283	16.3	380	2	A48227	kappa opioid recep
35	282	16.3	380	2	S36143	kappa opioid recep
36	282	16.3	398	2	I56504	mu opioid recep
37	279.5	16.1	363	2	I57940	mu opioid recep
38	279.5	16.1	373	2	JC4162	somatostatin recep
39	279	16.1	391	2	A41795	p2y receptor - bov
40	279	16.1	391	2	C41795	somatostatin recep
41	279	16.1	391	2	A39297	somatostatin recep
42	275.5	15.9	356	2	S42086	Interleukin-8 rece
43	274	15.8	399	2	I48705	proteinase activat
44	272.5	15.7	360	2	A53611	Interleukin-8 rece
45	272	15.7	380	2	JC2434	kappa opioid recep

#### ALIGNMENTS

##### RESULT 1

B45680

G protein-coupled peptide receptor EBI 2 - human

C:Species: Homo sapiens (man)

C:Date: 21-Sep-1993 #sequence-revision 18-Nov-1994 #text-change 21-Jul-2000

C:Accession: B45680

R:Burkenbach, M.; Josefsen, K.; Valamanchi, R.; Lenolr, G.; Kleff, E.

J. Virol. 67, 2209-2220, 1993

A:Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-couple

A:Reference number: A45680; MUID:9318173

A:Accession: B45680

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-361 <BIR>

A:Cross-references: GB:108177; NID:9292056; PIDN:AAA35924.1; PID:9292057

A:Experimental source: B-Lymphocytes

A:Note: Sequence extracted from NCBI backbone (NCBIN:127096, NCBI:127097)

C:Superfamily: AMP receptor P2u

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 21.1% Score 365; DB 2; Length 361;

Best Local Similarity 27.2%; Pred. No. 3.9e-24;

Matches 88; Conservative 78; Mismatches 135; Indels 22; Gaps 7;

OY	23	QLVPEALYVVEFLGILNLTALVFWH----	IPSSFTIYIKNTLVADLIMTLPFK 78
DB	31	RIWPLHYSLVFIIGLGNLALVIVONRKINST--	LYSTNLVLSIDLFTTALPTR 87
OY	79	ILSDSLAPMQLAFVCRFSVFYEETMVGIVLGLIARDFLKIRPLNIFLKKPVF 138	
DB	88	IAYVAMGFMDRIGDALCRITALVYINTYAGVNMWCLSDRFIAVHPRLYNKKIRIEH 147	
OY	139	AKYVSIITWFFLPISLPNMI--LSNKEATPSSVYKCAKSLGKPLGKWHOMVNICOPIF 196	
DB	148	AKGQCFIWWIIVAEQTLPLDINPMKQEAERTICMEYRNEETKSLPW--ILGACPIGY 205	
OY	197	WTFEFLALVFYVYIAKVVYVSYSKSKDRKN--NKTKEGVFVYVVAVFVCFAPPHFARV 255	
DB	206	VLPILITILICYSQICCLFRTAKONPLTEKSGVKKALNTIILIVVFLCFTPYHAI 265	
OY	256	PYTHSQT--NNKTCRLQNLDTAKETTLFLAATNLCMDPLIYIFLCKKFTKLPQMOGR 313	
DB	266	OHMIKRLRFNSNLECSGRHSFQISLHFTVCLMNPNCMDPIFFPACGKRVVMRLKR 325	
OY	314	KTTAS-----SQENHSSQTD 328	
DB	326	QVSVSISAVKSAPEENSRMTE 348	

##### RESULT 2

A40191

platelet-activating factor receptor - human

C:Species: Homo sapiens (man)  
C>Date: 28-Aug-1992 #sequence\_revision 28-Aug-1992 #text\_change 20-Jun-2000  
C:Accession: AA0191; JH0479; A41079; JCI359; A42831; I51923  
R:Kunz, D.; Gerard, N.P.; Gerard, C.  
J. Biol. Chem. 267, 9101-9106, 1992  
A>Title: The human leukocyte platelet-activating factor receptor. cDNA cloning, cell su  
A:Reference number: AA0191; MUID:92250505  
A:Accession: AA0191  
A:Molecule type: mRNA  
A:Residues: 1-342 <KUD>  
A:Cross-references: GB:M76674; NID:g456293; PIDN:AA60002.1; PID:g456294  
R:Ye, R.D.; Prossnitz, E.R.; Zou, A.; Cochrane, C.G.  
Biochem. Biophys. Res. Commun. 180, 105-111, 1991  
A>Title: Characterization of a human cDNA that encodes a functional receptor for platelet  
A:Reference number: JH0479; MUID:92028922  
A:Accession: JH0479  
A:Molecule type: mRNA  
A:Residues: 1-342 <YER>  
A:Cross-references: GB:M80436; NID:g189537; PIDN:AAA60001.1; PID:g189538  
A:Experimental source: granulocyte, cell line HL-60 cell  
R:Nakamura, M.; Honda, Z.; Izumi, T.; Sakenaka, C.; Mutoh, R.; Minami, M.; Bito, H.; Sey  
J. Biol. Chem. 266, 20400-20405, 1991  
A>Title: Molecular cloning and expression of platelet-activating factor receptor from hu  
A:Reference number: A41079; MUID:92041873  
A:Accession: A41079  
A>Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-342 <NAR>  
A:Cross-references: GB:D10202; GB:D90433; NID:g1997975; PIDN:AAA01050.1; PID:g219976  
R:Shigemoto, T.; Tsuchimoto, H.; McGregor, C.G.A.; Mutch, H.; Shimizu, T.; Kurochi, Y.  
Biochem. Biophys. Res. Commun. 189, 617-624, 1992  
A>Title: Molecular cloning and characterization of the platelet-activating factor recept  
A:Reference number: JCI359; MUID:93112021  
A:Accession: JCI359  
A:Molecule type: mRNA  
A:Residues: 1-315, 'N', 317-342 <SUG>  
A:Experimental source: heart  
A:NOTE: the authors translated the codon AAT for residue 316 as Lys  
R:Sejried, C.E.; Schweickart, V.L.; Godiska, R.; Gray, P.W.  
Genomics 13, 832-834, 1992  
A>Title: The human platelet-activating factor receptor gene (PTAFR) contains no introns  
A:Reference number: A42831; MUID:92347886  
A:Accession: A42831  
A:Molecule type: DNA  
A:Residues: 1-226, 'TG', 229-342 <SEX>  
A:Cross-references: GB:M88177; NID:g190697; PIDN:AAA60214.1; PID:g190698  
A:NOTE: sequence extracted from NCBI backbone (NCBIN:109813, NCBI:P.109814)  
R:Chase, P.B.; Halonen, M.; Regan, J.W.  
N. J. Respir. Cell Mol. Biol. 8, 240-244, 1993  
A>Title: Cloning of a human platelet-activating factor receptor gene: evidence for an in  
A:Reference number: I51923; MUID:93192035  
A:Accession: I51923  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-342 <RES>  
A:Cross-references: GB:S56396; NID:g298580; PIDN:AA625755.1; PID:g298581  
C:Genetics:  
A:Gene: GDB:PTAFR  
A:Cross-references: GDB:128806; OMIM:173393  
A:Map position: 1p35-1p34.3  
C:Superfamily: ATP receptor P2U  
C:Keywords: G protein-coupled receptor; transmembrane protein  
F:17-38/Domain: transmembrane #status predicted <TRI>  
F:54-75/Domain: transmembrane #status predicted <TRI>  
F:92-113/Domain: transmembrane #status predicted <TI>  
F:134-155/Domain: transmembrane #status predicted <TI>  
F:164-205/Domain: transmembrane #status predicted <TV>  
F:233-253/Domain: transmembrane #status predicted <TV>  
F:277-297/Domain: transmembrane #status predicted <VI>  
Query Match 19.4%; Score 336.5; DB: 2; Length 342;  
Best Local Similarity 26.2%; Pred. No. 1.1e-21;  
Matches 87; Conservative 75; Mismatches 137; Indels 33; Gaps 9;

```

0Y 18 DRIYQVPEPLLYTVVETLGLILMLALMVEVHPISSTF---IYLKNTLVADIDIMLM 74
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 10 DSEFRTYLPPIYSIIIFALGVANLYVMFAIRLPCCKKEFIKIFMNLTMADMLFIT 69
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 75 LPEKILSDSHLAPQOLRAFCVCFSSVIFYEMTVYGVILLGLIAPDRPLKTRPLNIFLK 134
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 70 LPLMYIYQONGNMTLLPFLCIVAGCLFFINTYCSVALGYITTYNRFOAVTRPIITAQAN 129
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 135 KPVFAKVSIFIFWELFELISLPMNLMSNKREATPSS-----VKKCAS--LKGBLGLKHMOM 187
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 130 TRKRGISLSIVYMAVGAASVFLLDSTNYPDSAGSGNTRYCEHNEKGSVP--LI 186
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 168 VNNICQELFTWVFIILMVEYVVIARKYVDSYRKSSKDKRKNKKLEGF---VFVYAVF 243
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 187 IHIFVFSEFLVELIILPCNLVIYITRL-----MQPVQOORNAEYKBRALMMVGCVLAVE 241
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 244 FVCFAPFHFAPVRYHSGTNNKTKDCLRONOLFIAKETTLFLAATNYICMDPLIYIFLCKKF 303
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 242 IICFYPHNHVQOLPWTIALGFO-DSEKHOAINDAQVTLCELLSTNCVLDPIVICYFLTKKF 300
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 304 ----TEKLPCKMOGRKTTASSOENHSORTDINT 331
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 301 RKHLTEKEYSMR-----SSRCKSRATTDIVYT 326
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 3
S13638
platelet-activating factor receptor - guinea pig
C:Species: Cavia porcellus (guinea pig)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 08-Oct-1999
A:Accession: S13638
R:Honda, Z.; Nakamura, M.; Miki, I.; Minami, M.; Watanabe, T.; Seyama, Y.; Okado, H.:
Nature 349, 342-346, 1991
A:Title: Cloning by functional expression of platelet-activating factor receptor from
A:Reference number: S13638; MIMD:01101726
A:Accession: S13638
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-342 <HON>
A:Cross-references: GB:556736; NID:g49442; PIDN:CAA40060.1; PID:g49443
A>Note: The species of guinea pig is not identified; in Genbank entry CCPAFREC, releas
A:Superfamily: ATP receptor p2u

```

Query Match	19.2%	Score 331.5	DB 2	Length 342
Best Local Similarity	27.9%	Pred. NO. 3e-21		
Matches 99	Conservative	65	Mismatches 128	Indels 63
				Gaps 15
QY	10	NRSECPDRTRIVOLFALYVTVVLGTLLMTLMAWVFI--PSG--STFIYIKNTLV	66	
Db	4	NSSRV--DSEERYTLFPIYYSIIPLVGLIANGVLMFARILYPERKKNLEIMVNLV	61	
QY	67	ADLIMTLMPKRIKLSDSLAPQOLRAEPCRSSVIFYETMYGIVLLGIADRELKIIR	126	
Db	62	ADLFLITLPLMIYYSNQGMMFLPKFELCNLAGCLFEIITYCSVAFGLYTTNRQAVKY	121	
QY	127	PLRNIEFLKRPFAKTVSFEIMFEL-----PESLPMNLSKKEATPSSVKCAS--LKG	178	
Db	122	PIKRAQATTKRRGIALSVIMVAIYAASVFLVMDSTNVASK--AGSGITRCFEPHEYG	180	
QY	179	PLGKMHQMVNNICOFI--FTVFIILMFLFYVVIARVDSYKSSKDRKN---NKKLEG	234	
Db	181	SKPV-----LIHICVLGFLFYELILFCNLVIYITLL-----RQVKKOQRNAEVRRLM	232	
QY	235	KVFVVAVAFVFCAPFHEBARVPYT-----HSQTNKTKDRCLONFLIAETLFL	283	
Db	233	MVCTVLAVFVFCFVBHMKVQLPMTLAEIGMPPSSNQAIND-----AQVYLIC	280	
QY	284	LAANINICMDPIITFLCKKF-----TEKLPQAO-----GRKTTASSQF-----NHS	334	
Db	281	LILSTNCVLDPIYIYELTKRFRKHLSEKTNINRSQKCSRVTYDTGETEALIDINT	335	

## RESULT 4

S43252

platelet-activating factor receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 20-Oct-1994 #sequence\_revision 10-Nov-1995 #text\_change 24-Nov-1999

C:Accession: S43252

R:Bito, H.; Honda, Z.; Nakamura, M.; Shimizu, T.

Eur. J. Biochem. 221, 211-218, 1994

A:Title: Cloning, expression and tissue distribution of rat platelet-activating-factor-

A:Reference number: S43252; MUID:94222063

A:Accession: S43252

A:Molecule type: mRNA

A:Residues: 1-341 &lt;BIT&gt;

A:Cross-references: GB:U04740; NID:94470384; PIDN:AAA18422.1; PID:94470385

C:Superfamily: ATP receptor P2u

Query Match 18.6%; Score 322.5; DB 2; Length 341;

Best Local Similarity 24.6%; Pred. No. 1.8e-20;

Matches 83; Conservative 77; Mismatches 147; Indels 31; Gaps 9;

JY 18 DTRVQVLPATVYVLTGLTMTLALMFVHI-PSS--STFIYIKNTLVADLIMTLM 74

DB 10 DSEFRTLPFIYVSVIVLVGVANGVYLMWFATLPSPKLMKIKIFVNTLVADLFLMT 69

QY 75 LPRKILSDSLAPMOLRAFCVCFSSVIFETMYGIVLGLIADRI.LKIRPLRNIFLK 134

DB 70 LPLMIYVYNSMGDMIVHFKLNCIAGCFFINTYCSVAFIYTTNRIOAVYPIKTAQAT 129

QY 135 KVPVAKTVSIFIMEFL-----FISLPMILSNKAPSSVYKCAISKPLG---LKHQ 186

DB 130 TRRGITLSIVIMISATASYFLATDSTNVPRKDGSGNTRCFEHKEPYSVPLVHI 189

QY 187 MVNNGOIFIMYFIL-MLVFYVIAKVDSTKSKSKDRKNKKI.BGKVFVAVAFV 245

DB 190 FITSCFFLVFELFYCNMVIHTLTPV---RQQRKPEVK--RALMVCYLAFAVFI 243

QY 246 CFAPFARVPYTHSQTNNKTCRLQNLFIKETTLPFLAATNICMPLIYFLCKPTE 305

DB 244 CFPHVHVQVLPMTLAEIGYQTN--FHQAINDAHOTLCLSTNCVLPVITCFLEKFRK 301

QY 306 KL-----PCMOGRKTTASSQENHSSQTDNITL 332

DB 302 HLESEKYSMRSSRKCRATSDTCETEVAMPANQTPVLSL 339

RESULT 5

S63666

platelet activating factor receptor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 20-Jun-2000

C:Accession: S63666

R:Shih, S.; Matsuda, Y.; Nakamura, M.; Waga, I.; Kume, K.; Izumi, T.; Shimizu, T.

Biochem. J. 314, 671-678, 1996

A:Title: A murine platelet-activating factor receptor gene: cloning, chromosomal localiz

A:Reference number: S63666; MUID:96239129

A:Accession: S63666

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-341 &lt;ISH&gt;

A:Cross-references: EMBL:D50872; NID:91256924; PIDN:BA04468.1; PID:91256925

C:Superfamily: ATP receptor P2u

Query Match 18.2%; Score 315.5; DB 2; Length 341;

Best Local Similarity 25.4%; Pred. No. 7.2e-20;

Matches 86; Conservative 77; Mismatches 144; Indels 31; Gaps 11;

QY 18 DTRVQVLPATVYVLTGLTMTLALMFVHI-PSS--STFIYIKNTLVADLIMTLM 74

DB 10 DSEFRTLPFIYVSVIVLVGVANGVYLMWFATLPSPKLMKIKIFVNTLVADLFLMT 69

QY 75 LPRKILSDSLAPMOLRAFCVCFSSVIFETMYGIVLGLIADRI.LKIRPLRNIFLK 134

DB 70 LPLMIYVYNSMGDMIVHFKLNCIAGCFFINTYCSVAFIYTTNRIOAVYPIKTAQAT 129

QY 135 KVPVAKTVSIFIMEFL-----FISLPMILSNKAPSSVYKCAISKPLGILKHMOMV 188

DB 130 TRRGITLSIVIMISATASYFLATDSTNVPRKDGSGNTRCFEHKEPYSVPLVHI 187

QY 189 NNICOFIFWTFEILMLVY---VVIAKVDYDSKSKDRKNKKLEGKVFVAVAFV 245

DB 188 HVTAFCEFLVF--FLIYCNLVIIHTLTPMRQRRAGVK--RRALMVCYLAFAVFI 243

QY 246 CFAPFARVPYTHSQTNNKTCRLQNLFIKETTLPFLAATNICMPLIYFLCKPTE 305

DB 244 CFPHVHVQVLPMTLAEIGYQTN--FHQAINDAHOTLCLSTNCVLPVITCFLEKFRK 301

QY 306 KL-----PCMOGRKTTASSQENHSSQTDNITL 332

DB 302 HLESEKYSMRSSRKCRATSDTCETEVAMPANQTPVLSL 339

RESULT 6

S15403

angiotensin II receptor type 1 - bovine

C:Species: Bos primigenius indicus x Bos primigenius taurus (cattle)

C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Nov-1999

C:Accession: S15403

R:Sasaki, K.; Yamano, Y.; Bardhan, S.; Iwai, N.; Murray, J.J.; Hasegawa, M.; Matsuda,

Nature 351, 230-233, 1991

A:Title: Cloning and expression of a complementary DNA encoding a bovine adrenal ang

A:Reference number: S15403; MUID:91251900

A:Accession: S15403

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-359 &lt;SAS&gt;

A:Cross-references: GB:X62294; NID:943; PIDN:CAA44182.1; PID:944

C:Superfamily: vertebrate rhodopsin

Query Match 17.9%; Score 309.5; DB 2; Length 359;

Best Local Similarity 26.1%; Pred. No. 2.5e-19;

Matches 90; Conservative 74; Mismatches 158; Indels 23; Gaps 10;

QY 1 MNTVMOGFNR-SERCPDRR--IVQVLPATVYVLTGLTMTL-ALMVFVHPISSST 56

DB 3 LNSSTEDGIRKIODCKRAGHNYIFIMIPYLSITIVVGISLVYIYIFMKLKV 62

QY 57 FIYKNTLVADLIMTLMPEKILSDSLAPMOLRAFCVCFSSVIFETMYGIVLGLI 116

DB 63 ASVFLNLALADLCFLTLPLMAVYTAEMEYRPGNYLCKIASASVFNLYASVELTCL 122

QY 117 AFDRFLKIRPLRNIFLKRPVATVSIPIWFELFISLPMILSNK---EATPSSVKKC 173

DB 123 SIDRYLAIVHPMKSRRLRMTLVAVTCIITLWLAGLASLPTIIRNVFTEMT--NTYVC 180

QY 174 A-----SLKGPLGLKHMOMVNNICOFIFWTFEILMLVYVIAKVDYDSKSKDRK 227

DB 181 AFHESQNSITLPVL---GLTKNLGLFL--PPIIITLSTILIKTKAKAEIOKNPKR 235

QY 228 NNKLESGVAVVAVAFVCFAPFARVPYTHSQTNNKTCRLQNLFIKETTLPFLAAT 287

DB 236 DD--IFKIIILAIIVLEFFFSWVPHQIFTFMDVLQGLIRCKIDVIDTAMPITICLAYF 293

QY 288 NICMDPLIYFLCKPTEK-LPCMOGRKTTASSQENHSSQTDNITL 331

DB 294 NNCINLPLFYGLGKFKKRYFLQLKTYIPRAKSHSNLSTKWSLS 338

RESULT 7

A48857

angiotensin II receptor type 1 - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 08-Oct-1999

C:Accession: A48857

R:Burns, K.D.; Inagami, T.; Harris, R.C.

Am. J. Physiol. 264, F645-F654, 1993

A:Title: Cloning of a rabbit kidney cortex AT1 angiotensin II receptor that is presen

Biochem. Biophys. Res. Commun. 183, 910-916, 1992

Article: Molecular cloning, sequence analysis and expression of a cDNA encoding human

A:Reference number: JH0267; MUID:92198490

A:Accession: JH0267

A:Molecule type: mRNA

A:Residues: 1-359 <TAK>

A:Experimental source: liver

R:Currow, K.M.; Pascoe, L.; White, P.C.

Mol. Endocrinol. 6, 1113-1118, 1992

Article: Genetic analysis of the human type-1 angiotensin II receptor.

A:Reference number: A44014; MUID:92375105

A:Accession: A44014

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-359 <CUR>

A:Cross-references: GB:M93394; NID:g178680; PID:g178681

A:Note: sequence extracted from NCBI backbone (NCBITN:111831, NCBIPI:111833)

C:Genetics:

A:Gene: GDB:AGT1

A:Cross-references: GDB:132359; OMIM:106165

A:Map position: 3q21-3q25

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; transmembrane

F:30-53/Domain: transmembrane #status predicted <TM1>

F:65-90/Domain: transmembrane #status predicted <TM2>

F:103-124/Domain: transmembrane #status predicted <TM3>

F:145-167/Domain: transmembrane #status predicted <TM4>

F:194-216/Domain: transmembrane #status predicted <TM5>

F:241-264/Domain: transmembrane #status predicted <TM6>

F:281-305/Domain: transmembrane #status predicted <TM7>

F:4,176,188/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 17.4%; Score 300.5; DB 2; Length 359;

Best Local Similarity 25.9%; Pred. No. 1.5e-18;

Matches 92; Conservative 71; Mismatches 137; Indels 35; Gaps 11;

1 MNTVVGQFNR-SERCPDTR-IVQVFPALYTVVLTGILNTL-ALWVFIHPSST 56

3 LNSTEDGDKRLQDDCPKGRHNTYIFWIPITLSIFVGFSGSLVYIYIFMKLT 62

57 FIYIKNLVADLIMTLMPKILSDSHLAPQLRAPVCRSSVIFETMYGVILGLI 116

63 ASVFLNALADLCFLTLPLMAVYTAEMYWMPGNYICKIASVSFNLASVFLTCL 122

117 AEDRLKIRPLRPLNFKKPVFAKTVSIFIFEFISLPMILSNK---EATSSVKKC 173

123 SIDRLIAVHMKSLKRLTMLVAKVTCIIIMLLGLASLPAITHRNPFIENT--NTVC 180

174 A-----SLKPLGLKMHQWNNICQEIFWTVETIMLVFYVIKRYDYSRKSQRK 227

181 AFHYESQNSTLPIDG---GLRKNILGFLF--PLLIIITSLYIMKAKKAYEIQKNPR- 234

228 NKKLEGVAVVAVVAVFYCFAPHFARVPYTHSQTNNKTDCLQNLQFIKETTFLAAT 287

235 -NDIFIKIIVAVIEFFFSWIPHOIFTEFLDVLQILIRDCRIADIVDFAMPITICIAVF 293

288 NICHDDIYIYIPLCKFTEKTLPCMOGRKTTASQENHSS-----QTDNIT 331

294 NNCINPLFYGLGKPF--KRYFDLNLKTIIPKAKSHSNLSTKMTSLSYRPSDVS 346

RESULT 9

S33733

G protein-coupled receptor - chicken

C:Species: Gallus gallus (chicken)

C:Date: 06-Jan-1995 #sequence, revision 06-Jan-1995 #text, change 24-Sep-1999

C:Accession: S33733

R:Webb, T.E.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burns

FEBS Lett. 324, 219-225, 1993

Article: Cloning and functional expression of a brain G-protein-coupled ATP receptor.

A:Reference number: S33733; MUID:93285340

A:Accession: S33733

A:Status: preliminary



## RESULT 12

15167  
 thrombin receptor - African clawed frog  
 C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 13-Sep-1996 #sequence, revision 13-Sep-1996 #text\_change 21-Jul-2000  
 C:Accession: 15167  
 R:Geertz, R.E.; Chen, J.; Ishii, M.; Ishii, K.; Nanev, T.; Turck, C.W.; Vu, T.H.; C  
 Nature 368, 648-651, 1994  
 A:Title: Thrombin receptor's specificity for agonist peptide is determined by its extrac  
 A:Reference number: 15167; MUID:94195429  
 A:Accession: 15167  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-420 <GER>  
 A:Cross-references: EMBL:009632; NID:9495197; PIDN:AAA18498.1; PID:9495198

Query Match 17.2%; Score 298.5; DB 2; Length 420;  
 Best Local Similarity 26.5%; Pred. No. 2,6e-18;

Matches 86; Conservative 61; Mismatches 131; Indels 47; Gaps 12;

OY 27 PALTYVFLTGILNTLAVF-----VHPSSTFIYLNKNTLVADLMTLMPKILS 81  
 DB 105 PSLITYVFLVGLPLMLALITLFLPKYAKKA---VYMLALADVFFVSVPFKIA- 159  
 OY 82 DSHLA--PMQLRAVCFRESSVIFEMVGIYGLIAFDFLKIIRPLNIFLKPPVA 139  
 DB 160 -YHLSGNDMLFGPGMCRIYTAIFCNMCSVLLIASISDRFLAVVYPMHSLSMTMSA 218  
 OY 140 KIVSIFVFEFFLISPMNLSNKENYPS-SVKKASLKGPLGLK--WHQVNNICQFLF 196  
 DB 219 YVACSEFIMLSIASITPLVPEOTKIPRLDITTCDDVLDLKDFFYYFSSCLLFF 278  
 OY 197 KTVFIMLVFYVIAKKVYDSYRSKSKDKRKNKLEGVF---VYVAVFECFEPHRA 253  
 DB 279 FVPIITITICIGT-----IRLSSSSIENSCKTRALFAVAVLCVFIICFEPYVL 331  
 OY 254 RVPYTHSOTNKTCDRLONQLEFIARETTLFLAATNIDPLIYFL---CKKFEKLPCM 310  
 DB 332 FLTHYLOEAN-----EFLYFAILSNACVGSVCCDPLIYYVASSCCQYKXLSLCC 383  
 OY 311 Q-----GRKT-----TASSQEHSS 325  
 DB 384 KIVSEPGSSTGQLMSTAMKNDNCST 408

## RESULT 13

544425  
 glotensin II receptor type 1 - dog  
 C:Species: Canis lupus familiaris (dog)  
 C:Date: 19-Mar-1997 #sequence, revision 19-Mar-1997 #text\_change 24-Nov-1999  
 C:Accession: S44425  
 R:Burns, L.; Clark, K.L.; Bradley, J.; Robertson, M.J.; Clark, A.J.L.  
 FEBS Lett. 343, 146-150, 1994  
 A:Title: Molecular cloning of the canine angiotensin II receptor. An AT1-like receptor  
 A:Reference number: S44425; MUID:94222188  
 A:Accession: S44425  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-359 <BUR>  
 A:Cross-references: PIDN:ABJ0674.1; PID:9546569  
 A:Experimental source: liver  
 C:Superfamily: vertebrate rhodopsin

Query Match 17.2%; Score 298; DB 2; Length 359;  
 Best Local Similarity 26.3%; Pred. No. 2.5e-18;

Matches 89; Conservative 69; Mismatches 136; Indels 24; Gaps 10;

OY 1 MNTVMQGNR-SERCPRDTR-IVQVFPALYVFLTGILNTL-ALMVFVHIPSSST 56  
 DB 3 LNSTEDDKIRIQDCCPRAGRNHYFVIMPLYSIIFVIGSLVIVYIFFMKLTIV 62  
 OY 57 FIIVKNTLVADLMTLMPKILSDSHLAPWQLRAVCFRESSVIFETMTVGIYVLLGLI 116

DB 63 ASVFELNLALADLCFLTLPLMAVYATAMEYRNPFGNYLCKIASASVFNLYASVFLITGL 122

OY 117 ADPRFKITRPLRNIFLKPVPFAKYVSIYWFLEPISLPMNLSK---EATPSSVKKC 173

DB 123 SIDRYVAIYHPKSPVRRITMLAKVCIIITWLAGIASLPTIIRHNVFIENF--NITVC 180

OY 174 A-----SLKGPLGKWHQVNNICQFIYFWFVFLMLVRYVYAKKYDSYRSKSKDKR 227

DB 181 AHYESQNSTLPIGL---GLTKNIGFLF--PLIITISYTLWTKLRAVEIQKKPR- 234

OY 228 NNKLEGVVVAVVAVFVCFAPFHFARVPYTHSOTNKTCDRLONQLEFIARETTLFLAAT 287

DB 235 -NDLFIKIMALVLFEEFVWYHQITFELDVLQGLIHDCKRADIVDRAVMPITICIAIF 293

OY 288 NTCMDPLIYIFLCKKFTKLPCKMGKRTTASSQEHSS 325

DB 294 NNCLNPLFYGFLGKRF--KKYFQLLKYIPRAKSSHS 329

## RESULT 14

UC2134  
 angiotensin II receptor type 1A - rat  
 N:Alternate names: AT1a receptor; AT3 receptor  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 28-Aug-1985 #sequence, revision 07-Oct-1994 #text\_change 24-Nov-1999  
 C:Accession: J02134; S15404; S20424; J01055  
 R:Conchou, S.; Monnot, C.; Strleix, M.E.; Bihoreau, C.; Corvol, P.; Clausen, E.  
 Biochem. Biophys. Res. Commun. 199, 1347-1354, 1994  
 A:Title: Synthetic cDNA encoding the rat AT1a receptor: a useful tool for structure-f  
 A:Reference number: J02134; MUID:94197726  
 A:Accession: J02134

A:Molecule type: mRNA  
 A:Residues: 1-359 <CON>  
 A>Note: the amino acid sequence of this protein is not given  
 R:Murphy, T.J.; Alexander, R.W.; Griendling, K.K.; Runge, M.S.; Bernstein, K.E.  
 Nature 351, 233-236, 1991

A:Title: Isolation of a cDNA encoding the vascular type-1 angiotensin II receptor.  
 A:Reference number: S15404; MUID:91251901

A:Accession: S15404

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-359 <MUR>

A:Cross-references: GB:X62295; NID:957773; PIDN:CAA44183.1; PID:957774

A:Experimental source: kidney

C:Superfamily: vertebrate rhodopsin

Keywords: G protein-coupled receptor; glycoprotein; GTP binding; receptor; transmem

F:27-86/Domain: transmembrane #status predicted <TM1>

F:103-123/Domain: transmembrane #status predicted <TM2>

F:147-167/Domain: transmembrane #status predicted <TM3>

F:195-218/Domain: transmembrane #status predicted <TM4>

F:240-263/Domain: transmembrane #status predicted <TM5>

F:278-289/Domain: transmembrane #status predicted <TM6>

F:4,176,188/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 17.2%; Score 297; DB 2; Length 359;



Best Local Similarity 26.6%; Pred. No. 3e-18;  
Matches 90; Conservative 67; Mismatches 157; Indels 24; Gaps 10.

```

QY 1 MATTVMQGNR--SEBQPROTR--IVOLVPAALYTVFELNGILLNT--ALMVFPHIISST 56
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db 3 LMSAEDGICKRQDDCPKAGRHSYIFVMIPITXISIEVVGIGNSLVIVIFYMKLV 62
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
QY 57 FIYUKNTLVADLIMTLMIPFKILSDSHLAPQURAFVOCRESSVIEYETMYGIVLGTI 116
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db 63 ASVELLNLALADCLCELLIPLMAVYTAMERYRPEGNHCLCKITASVSEMLIASVELLTCL 122
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
QY 117 AFDRELIKIIRPLNIFLKKPYEAKTVSIFIMFELEFISIPNNILSN:--EATPSVKKC 173
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db 123 SIDRYALIVHPKRSLSLRMLVAKVTCTIIMMAGIASLSPVHRYTIENT--NITWC 180
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
QY 174 A-----SLKGPGLGKHMOMVNNNICOFIFMVEFIIMLVFYVVIYAKKYDSYKRSKDRK 227
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db 181 AFHESRSNSTPIGL--GLAKNIGLFL--PFLIITLSTYLIMWAKKAYEIQKKPR- 234
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Y 228 NNKKLEGVFWVYVAFVFCFAFHFHARVPYTHSQNNKTKDCLONOJ.FIAKETTFLEAAT 287
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db 235 -NDOLFRIIMAVIEFFESWVPHQIFTEFLDVLIOGVHIDCKISDIYDTAMPITICIAF 293
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
QY 288 NICMDPLIYIFCKKFEKTEKLPOMOGKRTTASQEBHNS 325
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db 294 NNCNLNPLFYELGELKKE--KKYFLQLLKTIIPPAKSHSS 329
   |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|

```

## RESULT 15

150241 G:protein-coupled receptor 6H1 - chicken  
 N:Alternate names: purinoceptor 6H1  
 C:Species: Gallus gallus (chicken)  
 C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 02-Jun-2000  
 C:Accession: 150241; Jc4618  
 R:Kaplan, M.H.; Smith, D.I.; Sundick, R.S.  
 J:Immunol. 151, 628-636, 1993  
 A>Title: Identification of a G protein coupled receptor induced in activated T cells  
 A:Reference number: 150241; MUID:9332058  
 A:Accession: 150241  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-308 <KAP>  
 A:Cross-references: GB:006109; NID:g304383; PIDN:AAB06587.1; PID:g304384  
 R:Webb, T.E.; Kaplan, M.G.; Barnard, E.A.  
 Blochem. Biophys. Res. Commun. 219, 105-110, 1996  
 A>Title: Identification of 6H1 as a p2y purinoceptor: p2x5.  
 A:Reference number: Jc4618; MUID:96190677  
 A:Accession: Jc4618  
 A:Molecule type: mRNA  
 A:Residues: 1-308 <WEB>  
 A:Cross-references: GB:U06109; NID:g304383; PIDN:AAB06587.1; PID:g304384  
 A:Experimental source: T-cells  
 C:Comment: This receptor plays a role in T-cell activation.  
 C:Genetics:  
 A:Gene: p2x5  
 C:Superfamily: AMP receptor P2u  
 C:Keywords: G protein-coupled receptor; transmembrane protein  
 F:15-40/Domain: transmembrane #status predicted <TM1>  
 F:51-74/Domain: transmembrane #status predicted <TM2>  
 F:89-109/Domain: transmembrane #status predicted <TM3>  
 F:133-153/Domain: transmembrane #status predicted <TM4>  
 F:177-201/Domain: transmembrane #status predicted <TM5>  
 F:227-248/Domain: transmembrane #status predicted <TM6>  
 F:269-292/Domain: transmembrane #status predicted <TM7>

[illegible]

Search completed: October 11, 2002, 14:50:25  
Job time : 24 secs

Query Match	17.1%	Score 296.5	DB 2	Length 308
Best Local Similarity	24.3%	Pred. No 2.9e-18		
Matches 71	Conservative 66	Mismatches 144	Indels 9	Gaps 5

  

QY	12	SERPRTRIVQLVFPALTYWVFETGLTLNTLAIMVF--VHIDSSFTIYLKNTLVAD	68
		:::::::::::::::::::::	:
DB	3	SSNSTDSDFRITLYGGCVFSLGIANCAVALITFFTLKVNETP--PYMNLIAASD	60
		:::::::::::::::::::::	:

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2002, 14:47:00 ; Search time 30 seconds  
(without alignments)  
1920.244 Million cell updates/sec

Title: US-09-924-125-2

Perfect score: 1731  
Sequence: 1 MPTVYMGFNRSEKCPDRTR.....KTTASSQENHSQTDNITIG 333

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: SP:archaea:\*  
2: SP:bacteria:\*  
3: SP:fungi:\*  
4: SP:human:\*  
5: SP:invertebrate:\*  
6: SP:mammal:\*  
7: SP:mhc:\*  
8: SP:organelle:\*  
9: SP:phage:\*  
10: SP:plant:\*  
11: SP:rodent:\*  
12: SP:virus:\*  
13: SP:vertebrate:\*  
14: SP:unclassified:\*  
15: SP:viirus:\*  
16: SP:bacteriap:\*  
17: SP:archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1731	100.0	333	4 Q9BPV8	Q9BPV8 homo sapien
2	1366	78.9	337	11 Q9D812	Q9D812 mus musculu
3	1128	65.2	228	6 Q9BE53	Q9BE53 macaca fasc
4	928	53.6	176	4 Q9BY61	Q9BY61 homo sapien
5	833	48.1	342	6 Q95KC3	Q95KC3 macaca fasc
6	830	47.9	342	6 Q9BGT8	Q9BGT8 macaca fasc
7	829	47.9	342	4 Q9H244	Q9H244 homo sapien
8	813	47.0	347	11 Q9CPV9	Q9CPV9 mus musculu
9	807	46.6	343	11 Q9EPX4	Q9EPX4 mus musculu
10	767.5	44.3	338	11 Q9ESG6	Q9ESG6 mus musculu
11	692.5	40.0	358	4 Q9BY21	Q9BY21 homo sapien
12	692.5	40.0	358	4 Q96JZ8	Q96JZ8 homo sapien
13	681.5	39.4	359	11 Q99MT7	Q99MT7 mus musculu
14	541.5	31.3	269	4 Q9BXC2	Q9BXC2 homo sapien
15	363.5	21.0	367	4 Q9UE21	Q9UE21 homo sapien
16	339.5	19.6	337	4 Q91271	Q91271 homo sapien

17	337.5	19.5	340	6 Q95N02	Q95N02 sus scrofa
18	331	19.1	342	6 Q9GR76	Q9GR76 capra hircu
19	330.5	19.1	298	4 Q9UD26	Q9UD26 homo sapien
20	326	18.8	342	6 Q9XSD4	Q9XSD4 sus scrofa
21	326	18.8	342	6 Q9TYT5	Q9TYT5 bos taurus
22	320.5	18.5	339	11 Q924T8	Q924T8 ratu
23	318.5	18.4	339	11 Q9J471	Q9J471 mus musculu
24	318.5	18.4	352	11 Q99J74	Q99J74 mus musculu
25	315.5	18.2	352	11 Q9XK47	Q9XK47 mus musculu
26	310.5	17.9	296	6 Q9TYT6	Q9TYT6 canis fami
27	310.5	17.9	361	11 Q9J471	Q9J471 mus musculu
28	304.5	17.6	359	6 Q9N0U1	Q9N0U1 ovis arie
29	304	17.6	359	11 Q9BEP3	Q9BEP3 cavia porce
30	303.5	17.5	361	11 Q95B11	Q95B11 ratu
31	302	17.4	377	13 Q98U14	Q98U14 brachydanio
32	301.5	17.4	359	6 Q9GLN9	Q9GLN9 pan troglod
33	300	17.3	373	13 Q957S5	Q957S5 brachydanio
34	300	17.3	374	13 Q957A6	Q957A6 melagris g
35	298	17.2	380	13 Q9DG06	Q9DG06 carassius a
36	295.5	17.1	360	6 Q9BG77	Q9BG77 pan troglod
37	293.5	17.0	361	13 Q9OX57	Q9OX57 xenopus lae
38	293	16.9	400	6 Q95M54	Q95M54 macaca fasc
39	292	16.9	454	4 Q9H573	Q9H573 homo sapien
40	290	16.8	362	11 Q9JLZ0	Q9JLZ0 ratu
41	290	16.8	362	11 Q9JLW0	Q9JLW0 mus musculu
42	289.5	16.7	383	13 Q43324	Q43324 catostomus
43	287	16.6	359	11 Q9EOR3	Q9EOR3 meriones un
44	287	16.6	400	6 Q9MTW9	Q9MTW9 macaca mula
45	286	16.5	393	11 Q9R1M0	Q9R1M0 mus musculu

#### ALIGNMENTS

RESULT 1  
Q9BPV8  
ID Q9BPV8 PRELIMINARY; PRT; 333 AA.  
AC Q9BPV8;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE PUTATIVE G-PROTEIN-COUPLED RECEPTOR FKSG77 (G-PROTEIN COUPLED RECEPTOR  
DE GPR86) (G PROTEIN-COUPLED RECEPTOR) (G PROTEIN-COUPLED RECEPTOR  
DE GPR86).  
GN FKSG77 OR GPR86 OR GPR94.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=HEART;  
RA Wang Y., Gong L.;  
RT "Molecular cloning of FKSG77, a novel gene encoding a putative G-  
RT protein-coupled receptor.";  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
[2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21172992; PubMed=11273702;  
RA Wittenberger T., Schaller H.C., Hellebrand S.;  
RT "An expressed sequence tag (est) data mining strategy succeeding in  
RT the discovery of new G-protein coupled receptors.";  
RL J. Mol. Biol. 307:799-813(2001).  
[3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21458557; PubMed=11574155;  
RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vantl M.B., Arkhiko O.,  
RT Lewis T., Evans J.F., George S.R., O'Dowd B.F.;  
RT "Discovery and mapping of ten novel G protein-coupled receptor  
RL genes.";  
RL gene 275:83-91(2001).  
[4]  
RP SEQUENCE FROM N.A.

RA PubMed-11546776;  
 RA Commun D., Gonzalez N.S., Dethleux M., Brezillon S., Lannoy V.,  
 RA Parentier M., Boeynaems J.M.;  
 RT "Identification of a Novel Human ADP Receptor Coupled to G<sub>i</sub>.";  
 RA J. Biol. Chem. 276.41479-41485(2001).  
 DR EMBL: AF345565; AAK39068.1;  
 DR EMBL: AF295368; AAK01864.1;  
 DR EMBL: AF411113; AAL26484.1;  
 DR EMBL: AF406692; AAL01038.1;  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCR\_RHODPSN.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; UNKNOWN\_1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 DR KME Receptor.  
 SQ SEQUENCE 333 AA; 38440 MW; F234ABBS001D6F34 CRC64;  
 Query Match 100.0%; Score 1731; DB 4; Length 333;  
 Best Local Similarity 100.0%; Pred. No. 7.8e-147;  
 Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NNTTVMGSENRSEPCPRDTRIVQVLPALTYVFLTGILNTLALVWFHIPSSTFIY 60  
 DB 1 NNTTVMGSENRSEPCPRDTRIVQVLPALTYVFLTGILNTLALVWFHIPSSTFIY 60  
 QY 61 LKNTLVADLIMLMPFKILSDSHLAPWQRAFCRFSVIFETMYVIGVLLGLAFDR 120  
 DB 61 LKNTLVADLIMLMPFKILSDSHLAPWQRAFCRFSVIFETMYVIGVLLGLAFDR 120  
 QY 121 FLKTRPRLNIFLKKRPVAKTVSIFIMFELFISLPMNLSKKEATPSSVKKASLKP 180  
 DB 121 FLKTRPRLNIFLKKRPVAKTVSIFIMFELFISLPMNLSKKEATPSSVKKASLKP 180  
 QY 181 GIKHQMANNICQFLFTWVFLIMLVYVIAKVDYRSKSKDRKNNKLEGVVYV 240  
 DB 181 GIKHQMANNICQFLFTWVFLIMLVYVIAKVDYRSKSKDRKNNKLEGVVYV 240  
 QY 241 AVFVCFAPFHPARVPYHSHQNTNKTDCRLONOLEIAKETTLFLAATNICDPLIYIFLC 300  
 DB 241 AVFVCFAPFHPARVPYHSHQNTNKTDCRLONOLEIAKETTLFLAATNICDPLIYIFLC 300  
 QY 301 KKFTEKLPCMOGRKTTASSQENHSSQTDNTTLG 333  
 DB 301 KKFTEKLPCMOGRKTTASSQENHSSQTDNTTLG 333  
 RESULT 2  
 Q9DB12 PRELIMINARY; PRT; 337 AA.  
 Q9DB12 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE 2010001106RIK PROTEIN.  
 GN GPR86 OR 2010001106RIK.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID-10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-C57BL/6J; TISSUE-SMALL INTESTINE;  
 RX MEDLINE-21085660; PubMed-11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Katsukawa T., Saito R.,  
 RA Kato K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Peschle G., Quackenbush J.,  
 RA Schiraldi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Botfell D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustinchich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Waltz C., Whitaker C., Wilming L.,  
 RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuk S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 408:685-690(2001).  
 DR EMBL: AK008013; BAB25409.1;  
 DR MGI: MGI:1921441; Gpr86.  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCR\_RHODPSN.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; UNKNOWN\_1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 SQ SEQUENCE 337 AA; 38693 MW; 2C1A76FBE893D5EA CRC64;  
 Query Match 78.9%; Score 1366; DB 11; Length 337;  
 Best Local Similarity 77.5%; Pred. No. 3.1e-114;  
 Matches 259; Conservative 34; Mismatches 37; Indels 4; Gaps 3;  
 QY 1 NNTTVMGSENRSEPCPRDTRIVQVLPALTYVFLTGILNTLALVWFHIPSSTFIY 60  
 DB 5 INTTMOGSENRSEPCPRDTRIVQVLPALTYVFLTGILNTLALVWFHIPSSTFIY 64  
 QY 61 LKNTLVADLIMLMPFKILSDSHLAPWQRAFCRFSVIFETMYVIGVLLGLAFDR 120  
 DB 61 LKNTLVADLIMLMPFKILSDSHLAPWQRAFCRFSVIFETMYVIGVLLGLAFDR 124  
 QY 121 FLKTRPRLNIFLKKRPVAKTVSIFIMFELFISLPMNLSKKEATPSSVKKASLKP 180  
 DB 121 FLKTRPRLNIFLKKRPVAKTVSIFIMFELFISLPMNLSKKEATPSSVKKASLKP 183  
 QY 181 GIKHQMANNICQFLFTWVFLIMLVYVIAKVDYRSKSKDRKNNKLEGVVYV 240  
 DB 181 GIKHQMANNICQFLFTWVFLIMLVYVIAKVDYRSKSKDRKNNKLEGVVYV 242  
 QY 241 AVFVCFAPFHPARVPYHSHQNTNKTDCRLONOLEIAKETTLFLAATNICDPLIYIFLC 300  
 DB 241 AVFVCFAPFHPARVPYHSHQNTNKTDCRLONOLEIAKETTLFLAATNICDPLIYIFLC 302  
 QY 301 KKFTEKLPCMOGRK--TTASSQENHSSQTDNTTL 332  
 DB 303 KKFTEKLPCMOGRKTTASSQENHSSQTDNTTL 336  
 RESULT 3  
 Q9BE53 PRELIMINARY; PRT; 228 AA.  
 Q9BE53 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE HYPOTHETICAL PROTEIN.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 CC Cercopithecoidea; Macaca.  
 OX NCBI\_TaxID-9541;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-FRONTAL CORTEX;  
 RA Oseada N., Hida M., Kusuda J., Tanuma R., Ieki K., Hirai M., Terao K.,  
 RA Suzuki Y., Sugano S., Hashimoto K.;  
 RT "Isolation of full-length cDNA clones from macaque brain cDNA  
 RT libraries.";  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB056816; BAB39342.1;  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCR\_RHODPSN.

DR PROSITE; PS00237; G-PROTEIN\_RECEP\_F1.1; UNKNOWN.1.  
 DR PROSITE; PS50262; G-PROTEIN\_RECEP\_F1.2; 1.  
 SO SEQUENCE 228 AA; 26356 MW; 4790755BEEED22C CRC64;

Query Match 65.2%; Score 1120; DB 6; Length 228;  
 Best Local Similarity 94.7%; Pred. No. 3.9e-93;  
 Matches 216; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 106 MYGIVLGLIAPDRFKIIRPLNFIKRPVFAKTVSIFIMFLEFSLNMLISNKEA 165  
 DB 1 MYGIVLGLIAPDRFKIIRPLNFIKRPVFAKTVSIFIMFLEFSLNMLISNKEA 60  
 QY 166 TPSSVKKCASLKGPLGKHMOMVNNICOFIMFVILMLVYVYIAKKVDSYKRSKSD 225  
 DB 61 TPSSVKKCASLKGPLGKHMOMVNNISQIFIMFVILMLVYVYIAKKVDSYKRSKSD 120  
 QY 226 RKNKKLEGVYVYVAFVFCFAPFHARVPYTHSQTNNKTDCLONOLFIAKETTFLEA 285  
 DB 121 RKNKKLEGVYVYVAFVFCFAPFHARVPYTHSQTNNKTDCLONOLFIAKETTFLEA 180  
 Y 286 ATNIDMDPLIYIFLCKKTEKLPCKMGRKTTASQENHSQTDNITIG 333  
 DB 181 ATNIDMDPLIYIFLCKKTEKLPCKMGRKTTASQENHSQTDNITIG 228

## RESULT 4

Q9BY61 PRELIMINARY; PRT; 176 AA.

DT 01-JUN-2001 (TReMBLrel. 17, Created)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE PUTATIVE G-PROTEIN-COUPLED RECEPTOR GPCR1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN  
 RP SEQUENCE FROM N.A.  
 RA Zhang W., Wan T., Cao X.;  
 RT "Molecular cloning of a probable G protein-coupled receptor with three  
 transmembrane domains";  
 RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF178982; AK18752.1;  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm.1.1  
 DR PRINTS: PR00237; GPCR\_RHODOPSN.  
 DR PROSITE: PS50262; G-PROTEIN\_RECEP\_F1.2; 1.  
 DR KW Receptor.  
 SO SEQUENCE 176 AA; 20194 MW; 352FDA2EA70EF9AD CRC64;

Query Match 53.6%; Score 928; DB 4; Length 176;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-75;  
 Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 MILSNKEATPSSVKKCASLKGPLGKHMOMVNNICOFIMFVILMLVYVYIAKKVDS 217  
 DB 1 MILSNKEATPSSVKKCASLKGPLGKHMOMVNNICOFIMFVILMLVYVYIAKKVDS 60  
 QY 218 YKRSKSKDRKNNKLEGVYVYVAFVFCFAPFHARVPYTHSQTNNKTDCLONOLFIA 277  
 DB 61 YKRSKSKDRKNNKLEGVYVYVAFVFCFAPFHARVPYTHSQTNNKTDCLONOLFIA 120  
 QY 278 KETTFLEATNTCMPLIYIFLCKKTEKLPCKMGRKTTASQENHSQTDNITIG 333  
 DB 121 KETTFLEATNTCMPLIYIFLCKKTEKLPCKMGRKTTASQENHSQTDNITIG 176

RESULT 5  
 Q95KC3 PRELIMINARY; PRT; 342 AA.  
 AC Q95KC3;  
 DT 01-DEC-2001 (TReMBLrel. 19, Created)

DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE HYPOTHEITICAL 39.5 KDA PROTEIN.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 OX NCBI\_TaxID=9541;  
 RN  
 RP SEQUENCE FROM N.A.  
 RA TISSUE-MEDULLA OBLGATA;  
 RC Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,  
 RA Suzuki Y., Sugano S., Hashimoto K.;  
 RT "Isolation of full-length cDNA clones from macaque brain cDNA  
 libraries";  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB062981; BAB60747.1;  
 DR Hypothetical protein.  
 KW  
 SO SEQUENCE 342 AA; 39479 MW; E93FC26BBF5EC4C CRC64;

Query Match 48.1%; Score 833; DB 6; Length 342;  
 Best Local Similarity 49.1%; Pred. No. 1.3e-66;  
 Matches 155; Conservative 57; Mismatches 102; Indels 2; Gaps 1;

QY 15 CPRDRIYQVLPALYVYVFLGLINTLALVYVHPSSSTFIYIKNTVADLINTLM 74  
 DB 17 CTRDRIYQVLPALYVYVFLGLINTLALVYVHPSSSTFIYIKNTVADLINTLM 76  
 QY 75 LPEKILSDSLAPQLNAFVCFSSVIFETMYGVYVGLIAPDRFKIIRPLNFIK 134  
 DB 77 FPEKILSDSLAPQLNAFVCFSSVIFETMYGVYVGLIAPDRFKIIRPLNFIK 136  
 QY 135 KPVAKVSIITWFLFISLPMNLSNKEATPSSVKKCASLKGPLGKHMOMVNNICOF 194  
 DB 137 NLGAKLISVLINAFMFLSLPMNLSNKEATPSSVKKCASLKGPLGKHMOMVNNICOF 196  
 QY 195 IFMTVFLMLVYVYVAFVFCFAPFHARVPYTHSQTNNKTDCLONOLFIAKETTFLEA 254  
 DB 197 IFMTVFLMLVYVYVAFVFCFAPFHARVPYTHSQTNNKTDCLONOLFIAKETTFLEA 256  
 QY 255 VPTYHSQTNNKTDCLONOLFIAKETTFLEATNTCMPLIYIFLCKKTEKLPCKMGRKTTASQENHSQTD 312  
 DB 257 IPTYHSQTNNKTDCLONOLFIAKETTFLEATNTCMPLIYIFLCKKTEKLPCKMGRKTTASQENHSQTD 316  
 QY 313 RKTASQENHSQTD 328  
 DB 317 NSATQSOSQDNKKKED 332

## RESULT 6

Q9BGT8 PRELIMINARY; PRT; 342 AA.

DT 01-JUN-2001 (TReMBLrel. 17, Created)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE HYPOTHEITICAL 39.5 KDA PROTEIN.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 OX NCBI\_TaxID=9541;  
 RN  
 RP SEQUENCE FROM N.A.  
 RA TISSUE-FRONTAL LOBE LEFT;  
 RC Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,  
 RA Suzuki Y., Sugano S., Hashimoto K.;  
 RT "Isolation of full-length cDNA clones from macaque brain cDNA  
 libraries";  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB056385; BAB3041.1;  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm.1.1.



RA	Suzuki H., Toyooka K., Wang KH., Weitz C., Whitaker C., Wilmig L.
RA	Myshen-Boris A., Yoshida K., Haasegawa Y., Kawaji H., Kohetsuki S.,
RA	Hayashizaki T.,
RT	"Functional annotation of a full-length mouse cdna collection.";
RL	Nature 409:685-690(2001).
DR	EMBL; AK014807; BAB29561.1; -
DR	EMBL; AK013804; BAB29000.1; -
DR	MGI; MGI:1918089; p2ry12.
DR	MGI; MGI:1920308; 2900079922Rlx.
DR	InterPro; IPR000276; GPCR_Rhodopsn.
DR	Pfam; PF00001; 7tm_1; 1.
DR	PRINTS; PR00237; GPCRRHODOPSN.
DR	PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
SO	SEQUENCE 347 AA; 39473 MW; F10748B8E57E025F1 CRC64;
 Query Match            47.0%; Score 813; DB 11; Length 347; Best Local Similarity    47.8%; Pred. No. 7,8e-65; Matches 155; Conservative 56; Mismatches 107; Indels 6; Gaps	
Y	2 NTTWQGNBSEKRPDTRIVQLVPALYYVETLGLNTLAWLVHPSSSTFIYL 61         : : :         : : :         : : :         : : :
Dd	12 NTPSPG--TSTLCVRDVKIKIQVFPLLYTFELFAGATLSLARIRPFQRKSNIIFL 69 
Oy	62 KNTLVADIMLMPEKLISDSHLAPQOLAFVORESSVFEENMYGYLLGIAEDF 121       : : :
Dd	70 KNVIYSIDLMLITPEPKILSDAKGAGPLFLVCQVTSVFETFMXISIFLIITIDRY 129       : : :
Oy	122 LKIIRPLENLIPKKRPVAKVTISIFIMEFLFESIPNNIISNKKEATPSVKCASLNGPIG 181         : : :     : : :         : : :         : : :         : : :
Dd	130 LKTRREFPTSSPNULGAKILSYIAFMFLISPMMILNRKPKDVTKCSFLSERG 189 
Oy	182 LKHOMVNNICQIFETWVFILMVFYVVIARKYVDSYRSKSKDRKNKKLEGVVVVA 241 
Dd	190 LVMEHIYVICOVFWMFINFLIVCYSLIKRELYRSVTRGSAAKVKKVNVKFIIIA 249 
Oy	242 VEFCEPAFHFAHARPYNHSOTNNKTCDRLNOFLIAKETLFLAANRICMDPLITYFLCK 301 
Dd	250 VEEICEPVEFHARIPYLSOTRAVEDSAENTLEYEKESTLMTLSNACDPPIYEFLLCK 309 
Oy	302 KF---TEKLPCMGRKRTYASSO 321 
Dd	310 SFRRSLTSMLRCSNSTSGTNKK 333 
 RESULT 9	
G9EPX4	PRELIMINARY; PRT; 343 AA.
ID	09EPX4
AC	09EPX4:
DT	01-MAR-2001 (TREMBLrel. 16, Created)
DT	01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT	01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE	P2Y12 PLATELET ADP RECEPTOR.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCBI_TaxID=10116;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=SPRAGUE-DAWLEY.
RX	MEDLINE=21037966; PubMed=11196645;
RA	Hollinger G., Jantzen H.-M., Vincent D., Li G., England L.,
RA	Ramakrishnan V., Yang R.-B., Nurdan P., Nurdan A., Julius D.J.,
RA	Conley P.B.,
RT	"Identification of the Platelet ADP Receptor Targeted by
RT	Antithrombotic Drugs,"
RL	Nature 409:202-207(2001).
DR	EMBL; AF313450; AAG48943.1; -
DR	InterPro; IPR000276; GPCR_Rhodpsn.
DR	Pfam; PF00001; 7tm_1; 1.
DR	PRINTS; PR00237; GPCRRHODOPSN.
DR	PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KM	Receptor.
SO	SEQUENCE 343 AA; 39047 MW; 7AE0ACE66674136 CRC64;

	Query Match	46.6%	Score 807;	DB 11;	Length 343;
	Best Local Similarity	47.2%;	Pred. No. 2.6e-64;		
	Matches 151;	Conservative 60;	Mismatches 107;	Indels 2;	Gaps 1.
OY	2 NTTWOGFNKRSERCPDTRIVOLVPALTYVFLNGILLNTLNLTAANVFHIPSSFTIYLKNITLVADILM				
Db	12 NTSING--TSLGCSNDXYKITQVLPLLTVTVEFALLINLSLAMRFQQIRSNSTIFLL				
OY	62 KNTLVADILMTLMIPKKIISDSHLAPWOLAFAVCGRSSVIFFETMYGVIGLVGLAFDFR				
Db	70 KNATVIDLMLITFEPPKIISDAKLGGHRTLYLCQVTSVTFEFTMYISISFGILTIDRY				
OY	122 LKTIRLRNLIPLKKPFPAKVTSIIFFELPFISSLPMIISNKNEATPSVKCAASKLPKG				
Db	130 LKTTREFPKSSSNNLGAKITSLVAIAFMFLSLSPMIILTNRPDKDDTKCFSFKSEFG				
OY	182 LKHOMANNICOFIEFTVTILMLVFPVVLAKKYDYSRKSKSDRKRNKKLEGKFVVYA				
Db	190 LVWHIELVNYICOVIMINFLIYVCCLTLKEIKRYRVATRGSAAKPKRNVINKVFIITA				
OY	242 VEFVFCARPHFRAPVPTHSQTNKKTDCLRLONFLFAKETTELPLAATNICMDPLYIFIICK				
Db	250 VEFICVPPHPHFARIPTLTQTAVEDCNMENTLFYVEESTLMTLSLNACLDPEIFYEFFCK				
OY	302 KFTEKLPCMOGRKRTASSOE	321			
Db	310 SFRNSLMRLRCSTSGANKK	329			
	RESULT 10				
	QGSEG6				
ID	QGSEG6	PRELIMITARY;	PRT:	338 AA.	
AC	QGSEG6:				
DT	01-MAR-2001 (TREMBLrel. 16, Created)				
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)				
DT	01-JUN-2001 (TREMBLrel. 17, last annotation update)				
DE	7 TRANSMEMBRANE G-PROTEIN COUPLED RECEPTOR.				
OC	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI_Taxid	10090;				
RN	[1]				
RA	SEQUENCE FROM N.A.				
RA	Lee B.C., Scadden D.T.;				
RT	"7 transmembrane g protein coupled receptor from hematopoietic progenitors."				
RL	Submitted (Aug-1999) to the EMBL/Genebank/DDBJ databases.				
DR	EMBL: AF177211; AACG09275.1.-				
DR	InterPro: IPR000276; GPCR_Rhodopsn.				
DR	Pfam: PF00001; 7tm_1.1.				
DR	PRINTS: PR00237; GPCRHHODOPSN				
KW	PROSITE: PS50262; G-_PROTEIN_RECEP_F1.2; 1.				
KW	Receptor; Transmembrane.				
SQ	SEQUENCE 338 AA; 38861 MM; 4376B50622A68AAE CRC64;				
	Query Match	44.3%;	Score 767.5;	DB 11;	Length 338;
	Best Local Similarity	43.2%;	Pred. NO. 8.8e-61;		
	Matches 142;	Conservative 64;	Mismatches 112;	Indels 11;	Gaps 3;
OY	12 SERCRPDRIVOLVPALTYVFLNGILLNTLNLTAANVFHIPSSFTIYLKNITLVADILM				
Db	11 NOPCGMNIILTIKOIPIPVXAGNFITGLLNGISGHIEFYVSSSFITYLKNIIVADIDL				
OY	72 TLMPFKILSDSHLAPWOLAFAVCGRSSVIFFETMYGVIGLVGLAFDPFLKIIRPLENI				
Db	71 GLTFEPKVLGDGSCGMQVNVECVSAVIFYVMNYAISIVEFGILSPRRYYKYKPLITS				
OY	132 FLKPFVFXKTVSIPIWFLEFISLPNMILSKNEATPSSVKKCASIKGFLGKMHOMVANI				
Db	131 IVOSVNSKSLISVLAMTMLLAPNILITNQGVKEYTKICOMEKMKELGKRHKASNYI				
OY	192 CQEIFHWEIFIAMLVEYVVIAAKVDYSRKSQRKNKKILEGKVFVYVAVAFPCOAPFH				
Db	251				

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Db 191 EVSIFWVFLLLIVFYATATRTKIFSHLSKRNSTSVKRSKRNFISYLVFVGVCPYH 250
OY 252 FARVPYTHSOTNNKTKDCRLONOLFATKETTLLAATNICMDPIYFLCKKTE----- 305
Db 251 IARIPYKTSQTSCHSCKRKETLLAKETLLISAANVCLDPIYFFLCOPREVLNKKL 310
OY 306 --KLPCMOGRKTYTASSQEN--HSSQTDNI 330
Db 311 HMLKQVNDLEVSCKTKRENAIHES--TDFL 338

RESULT 11
O9BY21 PRELIMINARY; PRT; 358 AA.
AC O9BY21;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ORPHAN G PROTEIN-COUPLED RECEPTOR 87.
OX GPR87 OR GPR95.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21172992; PubMed=11273702;
RA Wittenberger T., Schaller H.C., Hellebrand S.;
RT "An expressed sequence tag (est) data mining strategy succeeding in
RT the discovery of new G-protein coupled receptors."
RL J. Mol. Biol. 307:799-813(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21458557; PubMed=11574155;
RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O.,
RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
RT "Discovery and mapping of ten novel G protein-coupled receptor
RT genes."
RL Gene 275:83-91(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF227763; AK01888.1; -
DR EMBL: AF411114; AA26485.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOODPSN.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL_1; 1.
DR PROSITE: PS50262; G-PROTEIN RECEPTOR FL_2; 1.
G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SEQUENCE 358 AA; 41435 MW; PDI57295BESD10F CRC64;

Query Match 40.0%; Score 692.5; DB 4; Length 358;
Best Local Similarity 41.0%; Pred. No. 4.6e-54;
Matches 125; Conservative 70; Mismatches 99; Indels 11; Gaps 3;

OY 10 NRSERCPDRTIVQ---LVFPAITYVFLTGILNTLALMTFVHIPSSSTIYIKNTL 65
Db 25 NRSDEPKNTLHNEFDIVLPVLYLIFVASILLGLAWMFIIRKTSIFELKNTIV 84
OY 66 VADLIMTLMPKILSDSHLAPMOLARAFVCRSSYIFETMVGVLGLIAFDREFKIT 125
Db 85 VADLIMTLMPKILSDSHLAPMOLARAFVCRSSYIFETMVGVLGLIAFDREFKIT 144
OY 126 RPLRNIFLKKPVFAKTVSIFIFLFFISLPNMLISNKEATPSSVKKCASLGPGLKWH 185
Db 145 KPFQDSRMVNTFTKVLSCVAVMAVLSLPNIIITNGOPTEDNIDHCKSLKSPGLKWH 204
OY 186 QMANNICQFIWTVFILMLVFLVYVIAKKVDSYR---SKSDRKNKKLEKGVVVAV 242
Db 205 TAVTVNSCLFPAVALVILIGCIYALSRIYHKSSROFISQSSIKRKHNSIR---VVAV 260
OY 243 FVVCAPRHPFARVPYTHSOTNNKTKDCRLONOLFATKETTLLAATNICMDPIYFLCKK 302

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Db 261 FETCELPYHLCRIPTFFSHLDRLDESAQKIYCKEITLFSACVNCIDPIYFPMCRS 320
OY 303 FTEKL 307
Db 321 FSRRL 325

RESULT 12
O96J28 PRELIMINARY; PRT; 358 AA.
AC O96J28;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE CDNA FL14878 FIS. CLONE PLACEL003238. WEAKLY SIMILAR TO PROBABLE
DE G PROTEIN-COUPLED RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Watanabe S., Hosokawa T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuno Y.,
RA Niimura K., Iwayanagi T.;
RT "NEBO human cDNA sequencing project."
RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AK027784; BAB55366.1; -
SEQUENCE 358 AA; 41462 MW; 7822700C8E3C7E9 CRC64;

Query Match 40.0%; Score 692.5; DB 4; Length 358;
Best Local Similarity 41.0%; Pred. No. 4.6e-54;
Matches 125; Conservative 70; Mismatches 99; Indels 11; Gaps 3;

OY 10 NRSERCPDRTIVQ---LVFPAITYVFLTGILNTLALMTFVHIPSSSTIYIKNTL 65
Db 25 NRSDEPKNTLHNEFDIVLPVLYLIFVASILLGLAWMFIIRKTSIFELKNTIV 84
OY 66 VADLIMTLMPKILSDSHLAPMOLARAFVCRSSYIFETMVGVLGLIAFDREFKIT 125
Db 85 VADLIMTLMPKILSDSHLAPMOLARAFVCRSSYIFETMVGVLGLIAFDREFKIT 144
OY 126 RPLRNIFLKKPVFAKTVSIFIFLFFISLPNMLISNKEATPSSVKKCASLGPGLKWH 185
Db 145 KPFQDSRMVNTFTKVLSCVAVMAVLSLPNIIITNGOPTEDNIDHCKSLKSPGLKWH 204
OY 186 QMANNICQFIWTVFILMLVFLVYVIAKKVDSYR---SKSDRKNKKLEKGVVVAV 242
Db 205 TAVTVNSCLFPAVALVILIGCIYALSRIYHKSSROFISQSSIKRKHNSIR---VVAV 260
OY 243 FVVCAPRHPFARVPYTHSOTNNKTKDCRLONOLFATKETTLLAATNICMDPIYFLCKK 302
Db 261 FETCELPYHLCRIPTFFSHLDRLDESAQKIYCKEITLFSACVNCIDPIYFPMCRS 320
OY 303 FTEKL 307
Db 321 FSRRL 325

RESULT 13
O99MT7 PRELIMINARY; PRT; 359 AA.
AC O99MT7;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE G-PROTEIN COUPLED RECEPTOR GPR87.

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GN GPR87.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-21172992; PubMed-11273702;  
RA Wittenberger T., Schaller H.C., Hallegrand S.;  
RT "An expressed sequence tag (est) data mining strategy succeeding in  
the discovery of new g-protein coupled receptors."  
RL J. Mol. Biol. 307:799-813(2001).  
CC -1 SUBCELLULAR LOCATION: INTERCAL MEMBRANE PROTEIN (BY SIMILARITY).  
DR EMBL: AF295366; AAK01866.1; -.  
DR MGD; MGI:1934133; Gpr87.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PS00237; GPCRRHODOPSN.  
JR PROSITE; P500237; G\_PROTEIN\_RECPT\_FL\_1; 1.  
JR PROSITE; P50262; G\_PROTEIN\_RECPT\_FL\_2; 1.  
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.  
SQ SEQUENCE 359 AA: 41462 MW; 2EB31C273EFCDEA CRC64;

Query Match 39.4%; Score 681.5; DB 11; Length 359;  
Best Local Similarity 42.2%; Pred. No. 4,4e+53;  
Matches 121; Conservative 62; Mismatches 97; Indels 7; Gaps 2;

OY 24 LVFPLVTVVFVTGLTLTALWLVFHIPSSSTFIYLKNTLLVALDITMLDPFKILLS 83  
DB 44 ILPLVLIVIFASILLNGLAWMIFPHIRNKTSIFYELKNIVADLTMTLPFRVIDA 103

OY 84 HLAPQLAPAFRESSVFEFTMYGVIGLIADRDRLKIIRPLRNLFLKPVAKYVS 143  
DB 104 GFGEPIFFETLCRIATSVLFANMYSIYFLGISIDRVLRKLKKVPGRSDSMYSTPTRYLS 163

OY 144 IFWFEEFLFISLPNMILSNKEATPSVSKCASLKGPLSLKHOMANNICQIFTFVFTLM 203  
DB 164 VCVVMYMALISPLNILLNGOPTKENIHDCMKSPCLAKMHMAVTYYDSCLFAVLVIL 223

OY 204 LVFYVIIVAkkkyydytkr---sksdKRNNKKLEGGKVVAVVFVCAPFHRPVTHS 260  
DB 224 IGCYIALISRHYIKKSROPFSOSSRRKRHNQSIIR---VVAVVEFGCPDYHCRIPTFS 279

OY 261 QTNKTDORLNOLFIKETLFLAATNICMDPLIYFLCKKFETE\_K 307  
DB 280 NLDRLLDESARKILYCKEMTFLSACNVCDPIIYFMCKSFSTRG 326

RESULT 14  
O9BXC2 PRELIMINARY; PRT; 269 AA.

AC O9BXC2  
DT 01-JUN-2001 (TREMBLrel, 17, Created)  
DT 01-JUN-2001 (TREMBLrel, 17, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel, 19, Last annotation update)  
DE PUTATIVE G-PROTEIN-COUPLED RECEPTOR FKG578 (G-PROTEIN-COUPLED RECEPTOR 87).

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiade; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=HEART;  
RA Wang Y.-g, Gong L.;  
RT "Identification of FKG578, a novel gene encoding a putative G-protein-coupled receptor."  
RL Submitted (Feb-2001) to the EMBL/GenBank/DDBJ databases.  
[2]

RN SEQUENCE FROM N.A.  
RP TISSUE=LUNG CARCINOMA, LARGE CELL UNDIFFERENTIATED?  
SC TISSUE=LUNG CARCINOMA, LARGE CELL UNDIFFERENTIATED?

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RA Strausberg R.;
RC Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RL -1- SUBCELLULAR LOCATION: INTERAL MEMBRANE PROTEIN (by SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF345566; AAK20069.1; -.
DR EMBL: BC009540; AAK09540.1; -.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1. 1.
DR PRINTS: PR00237; GPCR_RHODPSN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 269 AA; 31443 MW; 1E7D498E20717F6 CRC64;

Query Match 31.3%; Score 541.5; DB 4; Length 269;
Best Local Similarity 39.6%; Pred. No. 1.le-40;
Matches 95; Conservative 56; Mismatches 82; Indels 7; Gaps 2

OY 71 MTLMLPEKILSDSHLAPQOLRAFCVRESSVIFETMYVGIVLGLIAPRELIKIRPLRY 130
Db 1 MLLTPFRIVHAGRGPMFKFLICRYTVLRYANNYSIVFLGLISIDRYLVKVPFGD 60
OY 131 IFLKRPVEKATYSIFITWFLFSLPNMLISNKEATPSVSKKASLKGPLGKMHOMVNN 190
Db 61 SRNYSITFEKVLSCVGVWIMAVLSLPIILLTNGQFPEDINIHOSKSLSPGVKMHIAVRY 120
OY 191 ICGFLFWYFIIMLVFYVIAKVIDSYK---SKSKDRNNKKLEGVYVVVAFFVC 247
Db 121 VNSCFEVALVLLICLYIAISRYIHSSQFISQSSRRKKHNSIR---VVVAVFPEFC 176
OY 248 APFHARVAVYTHSQTNNNKDCRLQNLQNLFAKETTLFLATNTICMDPLIYIFICKRTEKL 307
Db 177 LPYHCRIPFTSHLDRLDESAOXILYICKETITFLSACNVCLEPIITFFMCRFSRRL 236

RESULT 15
O9UE21 PRELIMINARY; PRT; 367 AA.
AC O9UE21.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE P2Y-LIKE G-PROTEIN COUPLED RECEPTOR.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId:9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Blesius R.H., Weber R.G., Lichter P., Ogilvie A.;
RT "A novel orphan G-protein coupled receptor primarily expressed in the
RT brain is localized on human chromosomal band 2q21.";
RL J. Neurochem. 1998;1357-1365(1998).
DR EMBL: Y12546; CAAT3144.1; -.
DR HSSP: P34996; IDDD.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1. 1.
DR PRINTS: PR00237; GPCR_RHODPSN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
DR Receptor; G-protein coupled receptor.
SQ SEQUENCE 367 AA; 40989 MW; 132FBE97BE83C60C CRC64;

Query Match 21.0%; Score 363.5; DB 4; Length 367;
Best Local Similarity 27.7%; Pred. No. 1.le-24;
Matches 90; Conservative 69; Mismatches 137; Indels 29; Gaps 9;

OY 12 SERPDRIVQVLPALYVVEPLTGILNTALMVEVHISSST-FITYKNTLVADLI 70
Db 48 AEOGOEPEENMFASFYLLDFITALGNTLALMLFIRDKSGCPANVFLMHLAVADLS 107
OY 71 MTLMLPEKIL---SDSHAPQOLRAFCVRESSVIFETMYVGIVLGLIAPRELIKIRP 127

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Page 8

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